Mitra 10_627310 --STN History

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=> d his ful

     (FILE 'HOME' ENTERED AT 17:33:36 ON 21 OCT 2005)

     FILE 'REGISTRY' ENTERED AT 17:33:44 ON 21 OCT 2005

L1           95 SEA ABB=ON  PLU=ON  FHOS/BI

     FILE 'HCAPLUS' ENTERED AT 17:36:25 ON 21 OCT 2005

L2           29 SEA ABB=ON  PLU=ON  L1 OR FHOS
                D STAT QUE
                D IBIB ABS HITSTR L2 1-29

     FILE 'REGISTRY' ENTERED AT 17:37:32 ON 21 OCT 2005
L3          259 SEA ABB=ON  PLU=ON  FORMIN/BI

     FILE 'HCAPLUS' ENTERED AT 17:38:01 ON 21 OCT 2005
L4        44779 SEA ABB=ON  PLU=ON  L3 OR FORMIN
L5         1163 SEA ABB=ON  PLU=ON  L4(L)(?DIABET? OR INSULIN(2A)RESIS? OR
                ?GLYCEM?)
L6          796 SEA ABB=ON  PLU=ON  L4(L)(MRNA OR DNA OR ?NUCLE? OR PROTEIN)
L7           25 SEA ABB=ON  PLU=ON  L6 AND L5
L8           24 SEA ABB=ON  PLU=ON  L7 NOT L2
                D STAT QUE
                D IBIB ABS HITSTR L8 1-24
L10          11 SEA ABB=ON  PLU=ON  L4(L)SPLEEN
L11           6 SEA ABB=ON  PLU=ON  L10 NOT (L2 OR L8)
                D STAT QUE
                D IBIB ABS HITSTR L11 1-6
L12         183 SEA ABB=ON  PLU=ON  L4(L)GENE
L13          10 SEA ABB=ON  PLU=ON  L12 AND L5
L14           7 SEA ABB=ON  PLU=ON  L13 NOT (L2 OR L8 OR L11)
L15          87 SEA ABB=ON  PLU=ON  ("BROOKS CYDNEY C"/AU OR "BROOKS CYDNEY
                CAROLYN"/AU) OR BROOKS C/AU OR BROOKS C C/AU
L16          85 SEA ABB=ON  PLU=ON  L15 NOT (L2 OR L8 OR L11 OR L14)
L17          22 SEA ABB=ON  PLU=ON  L16 AND (L4 OR ?DIABET? OR INSULIN? OR
                ?GLYCEM? OR SPLEEN OR MRNA OR DNA OR ?NUCLE? OR PROTEIN OR
                GENE)

     FILE HOME

     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:   19 OCT 2005  HIGHEST RN 865652-03-5
     DICTIONARY FILE UPDATES:  19 OCT 2005  HIGHEST RN 865652-03-5

     New CAS Information Use Policies, enter HELP USAGETERMS for details.

     TSCA INFORMATION NOW CURRENT THROUGH JULY 14, 2005

       Please note that search-term pricing does apply when
       conducting SmartSELECT searches.

     ************************************************************
     *                                                          *
     * The CA roles and document type information have been removed from *
     * the IDE default display format and the ED field has been added,   *
```

* effective March 20, 2005. A new display format, IDERL, is now *
* available and contains the CA role and document type information. *
*
****

Structure search iteration limits have been increased. See HELP SLIMITS for details.

REGISTRY includes numerically searchable data for experimental and predicted properties as well as tags indicating availability of experimental property data in the original document. For information on property searching in REGISTRY, refer to:

http://www.cas.org/ONLINE/UG/regprops.html

FILE HCAPLUS

FILE COVERS 1907 - 21 Oct 2005 VOL 143 ISS 18
FILE LAST UPDATED: 20 Oct 2005 (20051020/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

This file contains CAS Registry Numbers for easy and accurate substance identification.

=>

```
=> fil hcaplus
FILE 'HCAPLUS' ENTERED AT 17:36:25 ON 21 OCT 2005
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.
COPYRIGHT (C) 2005 AMERICAN CHEMICAL SOCIETY (ACS)
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FILE COVERS 1907 - 21 Oct 2005  VOL 143 ISS 18
FILE LAST UPDATED: 20 Oct 2005  (20051020/ED)

New CAS Information Use Policies, enter HELP USAGETERMS for details.

 This file contains CAS Registry Numbers for easy and accurate
 substance identification.

=>
=> d stat que
L1            95 SEA FILE=REGISTRY ABB=ON  PLU=ON  FHOS/BI
L2            29 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L1 OR FHOS


=>
=> d ibib abs hitstr l2 1-29

L2   ANSWER 1 OF 29  HCAPLUS  COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER:         2005:999640  HCAPLUS
TITLE:                    Fhos2, a novel formin-related actin-organizing
                          protein, probably associates with the nestin
                          intermediate filament
AUTHOR(S):                Kanaya, Hideki; Takeya, Ryu; Takeuchi, Kosei;
                          Watanabe, Norinobu; Jing, Naihe; Sumimoto, Hideki
CORPORATE SOURCE:         Medical Institute of Bioregulation, Kyushu University,
                          3-1-1 Maidashi, Higashi-ku, Fukuoka, 812-8582, Japan
SOURCE:                   Genes to Cells (2005), 10(7), 665-678
                          CODEN: GECEFL; ISSN: 1356-9597
PUBLISHER:                Blackwell Publishing Ltd.
DOCUMENT TYPE:            Journal
LANGUAGE:                 English
AB   Fhos1 is a mammalian formin-family protein, and functions as an organizer
     of the actin microfilament.  Here we have cloned human and mouse cDNAs for
     a novel Fhos homolog, designated Fhos2.  The messages for Fhos2
     are expressed in the heart, kidney, and brain, where the Fhos1 mRNAs are
     not abundant.  Two splice variants of Fhos2 exist in a tissue-specific
     manner; the longer variant Fhos2L is the major form in the heart, whereas
     the kidney and brain predominantly express Fhos2S that encodes a shorter
     protein.  Over-expression of an active form of the two Fhos2 variants, as
     well as that of Fhos1, induces the formation of actin stress fibers in
     HeLa cells, suggesting that Fhos2 acts as an actin-organizing protein.
     Biochem. anal. using rat cardiomyoblastic H9c2 (2-1) cells reveals that
     endogenous Fhos2 is enriched in the intermediate filament fraction.
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Consistent with this, Fhos2 localizes to the nestin intermediate filament but not to other cytoskeletons, as demonstrated by staining of H9c2 (2 - 1) cells with anti-Fhos2 antibodies. Furthermore, Fhos2 is present in nestin-expressing neuroepithelial cells of the fetal rat brain. Thus, Fhos2 not only has the actin-organizing activity but also assocs. with nestin, which may imply a Fhos2-mediated link between the nestin intermediate filament and actin microfilament.

REFERENCE COUNT: 55 THERE ARE 55 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:409133 HCAPLUS
DOCUMENT NUMBER: 142:458904
TITLE: Sequences of **FHOS**-interacting proteins
INVENTOR(S): Sakamoto, Takeshi; Takeda, Shizu
PATENT ASSIGNEE(S): Japan
SOURCE: U.S. Pat. Appl. Publ., 163 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2005100966	A1	20050512	US 2004-805684		20040319
PRIORITY APPLN. INFO.:			US 2003-459936P	P	20030402
			US 2003-460103P	P	20030402
			US 2003-455766P	P	20030603

AB Novel protein-protein interactions have been discovered and confirmed using yeast two-hybrid system described herein. In particular, after studying the interacting ability of **FHOS** (bait) with random polypeptides expressed by anonymous cDNA libraries, it has been discovered that **FHOS** specifically interacts with proteins including GROUP1 (preys). Different fragments or domains of bait and prey proteins were also tested using yeast two-hybrid system to delineate domains or residues important for the interaction. Accordingly, this invention also discloses specific domains or fragments of **FHOS** capable of interacting with the specific domains or fragments of GROUP1. Methods of using the protein complexes in diagnosing diseases and disorders are also provided. In addition, the protein complexes are also useful in screening assays for identifying compds. effective in treating and/or preventing diseases and disorders associated with **FHOS** and its interactors.

IT **851503-85-0P 851503-86-1P 851503-87-2P**
851503-88-3P 851503-89-4P 851503-90-7P
851503-91-8P 851503-92-9P 851503-93-0P
851503-94-1P 851503-95-2P 851503-96-3P
851503-97-4P 851503-98-5P 851503-99-6P
851504-00-2P 851504-01-3P 851504-02-4P
851504-03-5P 851504-04-6P 851504-05-7P
851504-06-8P 851504-07-9P 851504-08-0P
851504-09-1P 851504-10-4P 851504-11-5P
851504-12-6P 851504-13-7P 851504-14-8P
851504-15-9P 851504-16-0P 851504-17-1P
851504-18-2P 851504-19-3P 851504-20-6P
851504-21-7P 851504-22-8P 851504-23-9P
851504-24-0P 851504-25-1P 851504-26-2P
851504-27-3P 851504-28-4P 851504-29-5P
851504-30-8P 851504-31-9P 851504-32-0P
851504-33-1P 851504-34-2P 851504-35-3P

851504-36-4P 851504-37-5P 851504-38-6P
851504-39-7P 851504-40-0P 851504-41-1P
851504-42-2P 851504-43-3P 851504-44-4P
851504-45-5P 851504-46-6P 851504-47-7P
851504-48-8P 851504-49-9P 851504-50-2P
851504-51-3P 851504-52-4P 851504-53-5P
851504-54-6P 851504-55-7P 851504-56-8P
851504-57-9P 851504-58-0P 851504-59-1P
851504-60-4P
RL: ANT (Analyte); BPN (Biosynthetic preparation); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation)
(amino acid sequence; sequences of **FHOS**-interacting proteins)

RN 851503-85-0 HCAPLUS
CN FHOS-interacting protein RNF 23 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-86-1 HCAPLUS
CN FHOS-interacting protein ERp59 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-87-2 HCAPLUS
CN FHOS-interacting protein BRD7 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-88-3 HCAPLUS
CN FHOS-interacting protein SPNA1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-89-4 HCAPLUS
CN FHOS-interacting protein VCP (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-90-7 HCAPLUS
CN FHOS-interacting protein STAT5A (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-91-8 HCAPLUS
CN FHOS-interacting protein TAKEDA009 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-92-9 HCAPLUS
CN FHOS-interacting protein PTRF (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-93-0 HCAPLUS
CN FHOS-interacting protein AK031693 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-94-1 HCAPLUS
CN FHOS-interacting protein 1200014P03Rik (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-95-2 HCAPLUS
CN FHOS-interacting protein NNP1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-96-3 HCAPLUS
CN FHOS-interacting protein LOC213473(195) (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-97-4 HCAPLUS
CN FHOS-interacting protein GOLGA3 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-98-5 HCAPLUS
CN FHOS-interacting protein MYGI (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-99-6 HCAPLUS
CN FHOS-interacting protein AK044679 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-00-2 HCAPLUS
CN FHOS-interacting protein RS21C6 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-01-3 HCAPLUS
CN FHOS-interacting protein KIAA0562 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-02-4 HCAPLUS
CN FHOS-interacting protein COPB (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-03-5 HCAPLUS
CN FHOS-interacting protein MYH7 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-04-6 HCAPLUS
CN FHOS-interacting protein MYH7 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-05-7 HCAPLUS
CN FHOS-interacting protein KIAA1633 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-06-8 HCAPLUS
CN FHOS-interacting protein KIAA1288 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-07-9 HCAPLUS
CN FHOS-interacting protein VCL (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-08-0 HCAPLUS
CN FHOS-interacting protein BC028274 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-09-1 HCAPLUS
CN FHOS-interacting protein BC028274 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-10-4 HCAPLUS
CN FHOS-interacting protein BC026864 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-11-5 HCAPLUS
CN FHOS-interacting protein 5730504C04Rik (mouse fragment) (9CI) (CA INDEX

NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-12-6 HCAPLUS
CN FHOS-interacting protein MYH9 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-13-7 HCAPLUS
CN FHOS-interacting protein p116Rip (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-14-8 HCAPLUS
CN FHOS-interacting protein TPM3 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-15-9 HCAPLUS
CN FHOS-interacting protein MYH6 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-16-0 HCAPLUS
CN FHOS-interacting protein MBLR (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-17-1 HCAPLUS
CN FHOS-interacting protein ZFP144 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-18-2 HCAPLUS
CN FHOS-interacting protein ZNF144 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-19-3 HCAPLUS
CN FHOS-interacting protein 14-3-3epsilon (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-20-6 HCAPLUS
CN FHOS-interacting protein 14-3-3epsilon (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-21-7 HCAPLUS
CN FHOS-interacting protein 14-3-3epsilon (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-22-8 HCAPLUS
CN FHOS-interacting protein BF672897(87) (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-23-9 HCAPLUS
CN FHOS-interacting protein CATNB (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-24-0 HCAPLUS
CN FHOS-interacting protein CATNS (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-25-1 HCAPLUS

CN FHOS-interacting protein SWAN (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-26-2 HCAPLUS
CN FHOS-interacting protein SWAN (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-27-3 HCAPLUS
CN FHOS-interacting protein 2300003P22 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-28-4 HCAPLUS
CN FHOS-interacting protein TAKEDA015 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-29-5 HCAPLUS
CN FHOS-interacting protein PCNT2 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-30-8 HCAPLUS
CN FHOS-interacting protein KPNA4 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-31-9 HCAPLUS
CN FHOS-interacting protein MAPKAP1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-32-0 HCAPLUS
CN FHOS-interacting protein TPT1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-33-1 HCAPLUS
CN FHOS-interacting protein AK014397 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-34-2 HCAPLUS
CN FHOS-interacting protein HRMT1L1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-35-3 HCAPLUS
CN FHOS-interacting protein HRMTIL1 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-36-4 HCAPLUS
CN FHOS-interacting protein SAT (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-37-5 HCAPLUS
CN FHOS-interacting protein BC023995 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-38-6 HCAPLUS
CN FHOS-interacting protein BC023995 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-39-7 HCAPLUS
CN FHOS-interacting protein TTN (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

RN 851504-40-0 HCAPLUS
CN FHOS-interacting protein LRRFIP1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-41-1 HCAPLUS
CN FHOS-interacting protein APC2 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-42-2 HCAPLUS
CN FHOS-interacting protein CYLN2 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-43-3 HCAPLUS
CN FHOS-interacting protein ACTN3 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-44-4 HCAPLUS
CN FHOS-interacting protein DTNBP1 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-45-5 HCAPLUS
CN FHOS-interacting protein TAKEDA013 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-46-6 HCAPLUS
CN FHOS-interacting protein 14-3-3g (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-47-7 HCAPLUS
CN FHOS-interacting protein 14-3-3zeta (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-48-8 HCAPLUS
CN FHOS-interacting protein 14-3-3zeta (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-49-9 HCAPLUS
CN FHOS-interacting protein 14-3-3zeta (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-50-2 HCAPLUS
CN FHOS-interacting protein 14-3-3b (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-51-3 HCAPLUS
CN FHOS-interacting protein 14-3-3theta (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-52-4 HCAPLUS
CN FHOS-interacting protein 14-3-3theta (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-53-5 HCAPLUS
CN FHOS-interacting protein SPNB2 (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-54-6 HCAPLUS
CN FHOS-interacting protein BC020494 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-55-7 HCAPLUS
CN FHOS-interacting protein MACF1 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-56-8 HCAPLUS
CN FHOS-interacting protein MYH1 (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-57-9 HCAPLUS
CN FHOS-interacting protein PPGB (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-58-0 HCAPLUS
CN FHOS-interacting protein ZYX (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-59-1 HCAPLUS
CN FHOS-interacting protein PRKCABP (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851504-60-4 HCAPLUS
CN FHOS-interacting protein MYLK (mouse fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **851503-75-8P**, Protein **FHOS** (human fragment)
851503-76-9P, Protein **FHOS** (human fragment)
851503-77-0P, Protein **FHOS** (human fragment)
851503-78-1P, Protein **FHOS** (human fragment)
851503-79-2P, Protein **FHOS** (human fragment)
851503-80-5P, Protein **FHOS** (human fragment)
851503-81-6P, Protein **FHOS** (human fragment)
851503-82-7P, Protein **FHOS** (human fragment)
851503-83-8P, Protein **FHOS** (human fragment)
851503-84-9P, Protein **FHOS** (human fragment)
RL: ARG (Analytical reagent use); BPN (Biosynthetic preparation); PRP (Properties); ANST (Analytical study); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; sequences of **FHOS**-interacting proteins)
RN 851503-75-8 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-76-9 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-77-0 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-78-1 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-79-2 HCAPLUS

CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-80-5 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-81-6 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-82-7 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-83-8 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
RN 851503-84-9 HCAPLUS
CN Protein FHOS (human fragment) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 3 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:394682 HCAPLUS
DOCUMENT NUMBER: 142:445550
TITLE: Gene expression profiles for the diagnosis and prognosis of breast cancer
INVENTOR(S): Erlander, Mark; Ma, Xiao-Jun; Wang, Wei; Wittliff, James L.
PATENT ASSIGNEE(S): Arcturus Bioscience, Inc. University of Louisville, USA
SOURCE: U.S. Pat. Appl. Publ., 40 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
US 2005095607	A1	20050505	US 2004-795092		20040305
PRIORITY APPLN. INFO.:			US 2003-453006P	P	20030307

AB The invention relates to the identification and use of gene expression profiles, or patterns, suitable for identification of breast cancer patient populations with different survival outcomes. The gene expression profiles may be embodied in nucleic acid expression, protein expression, or other expression formats, and may be used in the study and/or determination of the prognosis of a patient, including breast cancer survival.

L2 ANSWER 4 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:139371 HCAPLUS
DOCUMENT NUMBER: 142:195820
TITLE: Gene expression profiles and biomarkers for the detection of Chagas disease and other disease-related gene transcripts in blood
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.

SOURCE: U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004241729	A1	20041202	US 2004-813097	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2004241729	A1	20041202	US 2004-813097	20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-813097	A 20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular Chagas disease, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L2 ANSWER 5 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:139370 HCAPLUS
DOCUMENT NUMBER: 142:195819
TITLE: Gene expression profiles and biomarkers for the detection of Chagas disease and other disease-related gene transcripts in blood
INVENTOR(S): Liew, Choong-Chin
PATENT ASSIGNEE(S): Chondrogene Limited, Can.
SOURCE: U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 47
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE

US 2004241729	A1	20041202	US 2004-813097	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2004241729	A1	20041202	US 2004-813097	20040330

PRIORITY APPLN. INFO.:

US 1999-115125P	P	19990106
US 2000-477148	B1	20000104
US 2002-268730	A2	20021009
US 2003-601518	A2	20030620
US 2004-802875	A2	20040312
US 2004-813097	A	20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular Chagas disease, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L2 ANSWER 6 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2005:60760 HCAPLUS
Correction of: 2004:1036573

DOCUMENT NUMBER: 142:153477
Correction of: 142:16776

TITLE: Gene expression profiles and biomarkers for the detection of Chagas disease and other disease-related gene transcripts in blood

INVENTOR(S): Liew, Choong-Chin

PATENT ASSIGNEE(S): Chondrogene Limited, Can.

SOURCE: U.S. Pat. Appl. Publ., 154 pp., Cont.-in-part of U.S. Ser. No. 802,875.
CODEN: USXXCO

DOCUMENT TYPE: Patent

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 47

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004241729	A1	20041202	US 2004-813097	20040330
US 2004014059	A1	20040122	US 2002-268730	20021009
US 2005191637	A1	20050901	US 2004-803737	20040318
US 2005196762	A1	20050908	US 2004-803759	20040318
US 2005196763	A1	20050908	US 2004-803857	20040318
US 2005196764	A1	20050908	US 2004-803858	20040318
US 2005208505	A1	20050922	US 2004-803648	20040318
US 2004241729	A1	20041202	US 2004-813097	20040330

US 2004241729	A1	20041202	US 2004-813097	20040330
US 2004265869	A1	20041230	US 2004-812716	20040330
PRIORITY APPLN. INFO.:			US 1999-115125P	P 19990106
			US 2000-477148	B1 20000104
			US 2002-268730	A2 20021009
			US 2003-601518	A2 20030620
			US 2004-802875	A2 20040312
			US 2004-813097	A 20040330

AB The present invention is directed to detection and measurement of gene transcripts and their equivalent nucleic acid products in blood. Specifically provided is anal. performed on a drop of blood for detecting, diagnosing, and monitoring diseases, and in particular Chagas disease, using gene-specific and/or tissue-specific primers. Affymetrix Human Genome U133 and ChondroChip microarrays were used to detect differentially expressed gene transcripts in hypertension, obesity, allergy, systemic steroids, coronary artery disease, diabetes type 2, hyperlipidemia, lung disease, bladder cancer, rheumatoid arthritis, osteoarthritis, liver cancer, schizophrenia, Chagas disease, asthma, and manic depression syndrome. The present invention describes methods by which delineation of the sequence and/or quantitation of the expression levels of disease-specific genes allows for an immediate and accurate diagnostic/prognostic test for disease or to assess the effect of a particular treatment regimen. [This abstract record is one of 3 records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

L2 ANSWER 7 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:1060769 HCAPLUS
DOCUMENT NUMBER: 142:32987
TITLE: Methods for treating diabetes and insulin resistance by activating gene **FHOS** (Formin Homologue Overexpressed in Spleen) expression
INVENTOR(S): Brooks, Cydney C.
PATENT ASSIGNEE(S): AdipoGenix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 24 pp.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004248836	A1	20041209	US 2003-627310	20030725
PRIORITY APPLN. INFO.:			US 2002-401389P	P 20020805

AB Methods for treating diabetes and/or insulin resistance by administering an activator of **FHOS** (Formin Homolog Overexpressed in Spleen) are disclosed. **FHOS** is originally identified as a formin/diaphanous protein family member involved in cytokinesis and stress fiber formation and bridging Rho GTPase and Src tyrosine kinase signaling. The present invention discovered that **FHOS** expression is downregulated in the adipocytes of human subjects having diabetes and/or insulin resistance. Thus the present invention is directed to methods of increasing expression of **FHOS**, for example, in fat and/or muscle cells of diabetic and/or insulin resistant subjects as a therapeutic approach to treating said subjects. Suitable activators of **FHOS** which can be employed in the methods of the invention include, but are not limited to, a **FHOS** nucleic acid mol., a plasmid comprising a **FHOS** nucleic acid mol., a **FHOS** adenovirus, a **FHOS** retrovirus and a **FHOS** protein or biol. active

portion thereof. Suitable activators of **FHOS** further include, but are not limited to a protein or biol. active fragment thereof, a nucleic acid mol. or biol. active fragment thereof, an antibody or biol. active fragment thereof, a peptide, a peptidomimetic, a nonpeptide oligomer or small mol.

IT **804573-02-2P**
RL: BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(amino acid sequence; methods for treating diabetes and insulin resistance by activating gene **FHOS** (Formin Homolog Overexpressed in Spleen) expression)
RN 804573-02-2 HCAPLUS
CN Protein (human gene FHOS (Formin Homologue Overexpressed in Spleen)) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
IT **804573-01-1**
RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(nucleotide sequence; methods for treating diabetes and insulin resistance by activating gene **FHOS** (Formin Homolog Overexpressed in Spleen) expression)
RN 804573-01-1 HCAPLUS
CN DNA (human gene FHOS (Formin Homologue Overexpressed in Spleen) protein cDNA plus flanks) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 8 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:593252 HCAPLUS
DOCUMENT NUMBER: 141:312831
TITLE: EBV attachment stimulates **FHOS**/FHOD1 redistribution and co-aggregation with CD21: Formin interactions with the cytoplasmic domain of human CD21
AUTHOR(S): Gill, Michael B.; Roecklein-Canfield, Jennifer; Sage, David R.; Zambela-Soediono, Maria; Longtine, Nina; Uknis, Marc; Fingeroth, Joyce D.
CORPORATE SOURCE: Divisions of Infectious Diseases, Experimental Medicine, Harvard Medical School, Brigham and Women's Hospital, Boston, MA, 02115, USA
SOURCE: Journal of Cell Science (2004), 117(13), 2709-2720
CODEN: JNCSAI; ISSN: 0021-9533
PUBLISHER: Company of Biologists Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB CD21 is a multifunctional receptor for Epstein-Barr virus (EBV), for C3dg and for CD23. Upon engagement of immune complexes CD21 modulates immunoreceptor signaling, linking innate and adaptive immune responses. The mechanisms enabling CD21 to independently relay information between the exterior and interior of the cell, however, remain unresolved. The authors show that formin homolog overexpressed in spleen (**FHOS** /FHOD1) binds the cytoplasmic domain of human CD21 through its C terminus. When expressed in cells, EGFP-**FHOS** localizes to the cytoplasm and accumulates with actin in membrane protrusions. Plasma membrane aggregation, redistribution and co-localization of both proteins are stimulated when EBV (ligand) binds CD21. Though widely expressed, **FHOS** RNA is most abundant in the littoral cell, a major constituent of the red pulp of human spleen believed to function in antigen filtration. Formins are mol. scaffolds that nucleate actin by a

pathway distinct from Arp2/3 complex, linking signal transduction to actin reorganization and gene transcription. Thus, ligand stimulation of **FHOS**-CD21 interaction may transmit signals through promotion of cytoskeletal rearrangement. Moreover, formin recruitment to sites of actin assembly initiated by immunoreceptors could be a general mechanism whereby co-receptors such as CD21 modulate intracellular signaling.

REFERENCE COUNT: 64 THERE ARE 64 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

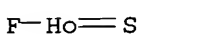
L2 ANSWER 9 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:573875 HCAPLUS
DOCUMENT NUMBER: 141:273253
TITLE: Riboproteomics of the Hepatitis C Virus Internal Ribosomal Entry Site
AUTHOR(S): Lu, Henry; Li, Weiqun; Noble, William Stafford; Payan, Donald; Anderson, D. C.
CORPORATE SOURCE: Rigel Inc., South San Francisco, CA, 94066, USA
SOURCE: Journal of Proteome Research (2004), 3(5), 949-957
CODEN: JPROBS; ISSN: 1535-3893
PUBLISHER: American Chemical Society
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Hepatitis C virus (HCV) protein translation is mediated by a cis-acting RNA, an internal ribosomal entry site (IRES), located in the 5' nontranslated region of the viral RNA. To examine proteins bound to the IRES, which could include proteins important for its function as well as potential drug targets, we used shotgun peptide sequencing to identify proteins in quadruplicate protein affinity exts. of lysed Huh7 cells, obtained using a biotinylated IRES. Twenty-six proteins bound the HCV IRES but not a reversed complementary sequence RNA or vector RNA controls. These included five ribosomal subunits, nine eukaryotic initiation factor 3 subunits, and novel interacting proteins such as the cytoskeletal-related proteins actin, **FHOS** (formin homolog overexpressed in spleen) and MIP-T3 (microtubule interacting protein that assocs. with TRAF3). Other novel HCV IRES-binding proteins included UNR (upstream of N-ras), UNR-interacting protein, and the RNA-binding proteins PAI-1 (plasminogen activator inhibitor-1) mRNA binding protein and Ewing sarcoma breakpoint 1 region protein EWS. A large set of addnl. proteins bound both the HCV IRES and a reversed complementary IRES sequence control, including the known HCV interactors PTB (polypyrimidine tract binding protein), the La autoantigen, and nucleolin. The discovery of these novel HCV IRES-binding proteins suggests links between IRES biol. and the cytoskeleton, signal transduction, and other cellular functions.

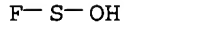
REFERENCE COUNT: 66 THERE ARE 66 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 10 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:528239 HCAPLUS
DOCUMENT NUMBER: 142:15688
TITLE: Formation of complex sulfofluorides of the structure type Yb3S2F4 in Ba(Eu)F2-rare earth sulfide-rare earth fluoride systems
AUTHOR(S): Zynchenko, V. F.; Efrudhina, N. P.; Bilyavina, N. M.; Stoyanova, I. V.; Stamikosto, O. V.; Markiv, V. Ya.
CORPORATE SOURCE: Fiz.-Khim. Inst. im. O. V. Bogats'kogo, NAN Ukr., Odessa, Ukraine
SOURCE: Ukrainskii Khimicheskii Zhurnal (Russian Edition) (2004), 70(5-6), 21-26
CODEN: UKZHAU; ISSN: 0041-6045
PUBLISHER: Institut Obshchei i Neorganicheskoi Khimii im. V. I.

Vernadskogo NAN Ukrainy
DOCUMENT TYPE: Journal
LANGUAGE: Ukrainian
AB Possibility of solid-state synthesis of complex sulfofluorides of Yb3S2F4 structural type in the systems BaF2-Ln2S3-LnF3 and EuS(EuF3)-Ln2S3-LnF3 (Ln = Y, La-Lu) was established. Their crystal lattices some differ in parameters in comparison with those for abnormal phases of simple sulfofluorides. The parameters' ration c/a regularly increases with decreasing of ionic radii of lanthanides from La to Tm. The character of diffusion reflection spectra indicates the valence state of Eu(II) and mixed-valence one for Nd, Sm, Dy, Tm in the complex sulfofluorides.
IT **25180-88-5**, Holmium fluoride sulfide (HoFS)
RL: RCT (Reactant); RACT (Reactant or reagent)
(reaction with europium monosulfide and rare earth fluoride/sulfide)
RN 25180-88-5 HCAPLUS
CN Holmium fluoride sulfide (HoFS) (8CI, 9CI) (CA INDEX NAME)



L2 ANSWER 11 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:363847 HCAPLUS
DOCUMENT NUMBER: 141:106160
TITLE: Classical versus redox tautomerism: substituent effects on the keto/enol and sulfoxide/sulfenic acid equilibria
AUTHOR(S): Alkorta, Ibon; Elguero, Jose
CORPORATE SOURCE: Instituto de Quimica Medica (CSIC), Madrid, E-28006, Spain
SOURCE: Tetrahedron Letters (2004), 45(21), 4127-4129
CODEN: TELEAY; ISSN: 0040-4039
PUBLISHER: Elsevier
DOCUMENT TYPE: Journal
LANGUAGE: English
AB MP2/6-311+G ab initio calcns. were carried out for a classical example of tautomerism, the keto/enol [RCOCH3/RC(OH)CH2] and an example of redox tautomerism, the sulfoxide/sulfenic acid [RS(O)H/RSOH]. Eleven R substituents were examined Both equilibrium show proportional energies and similar dependence on the Swain-Lupton and parameters.
IT **83045-12-9**, Fluorosulfoxylic acid
RL: CPS (Chemical process); PEP (Physical, engineering or chemical process); PRP (Properties); RCT (Reactant); PROC (Process); RACT (Reactant or reagent)
(classical vs. redox tautomerism and substituent effects on keto/enol and sulfoxide/sulfenic acid equilibrium)
RN 83045-12-9 HCAPLUS
CN Fluorosulfoxylic acid (9CI) (CA INDEX NAME)



REFERENCE COUNT: 9 THERE ARE 9 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 12 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:362522 HCAPLUS
DOCUMENT NUMBER: 141:88689

TITLE: Chiral discrimination and isomerization processes in monomers, dimers and trimers of sulfoxides and thioperoxides
AUTHOR(S): Alkorta, Ibon; Picazo, Oscar; Elguero, Jose
CORPORATE SOURCE: CSIC, Instituto de Quimica Medica, Madrid, E-28006, Spain
SOURCE: Tetrahedron: Asymmetry (2004), 15(9), 1391-1399
CODEN: TASYE3; ISSN: 0957-4166
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The chiral discrimination in cyclic dimers and trimers of mono-substituted sulfoxides and thioperoxides has been studied by means of DFT (B3LYP/6-31+G**) and ab initio (MP2/6-311+G**) calcns. In addition, the inter- and intramol. proton transfer processes that interconvert these two classes of compds. have been considered for the isolated mols. and clusters. The thioperoxide clusters are more stable than the corresponding sulfoxides even though the strongest hydrogen bonds are found in the latter complexes. Correlations have been found between the relative energies of the sulfoxide vs. the thioperoxide compds. and the transition state barriers. The geometry of the hydrogen bonds has been analyzed using a Steiner-Limbach relationship.

IT **83045-12-9**, Fluorosulfoxylic acid
RL: CPS (Chemical process); PEP (Physical, engineering or chemical process); PRP (Properties); RCT (Reactant); PROC (Process); RACT (Reactant or reagent)
(ab initio study of chiral discrimination and tautomerization in monomers dimers and trimers of sulfoxides and thioperoxides)

RN 83045-12-9 HCAPLUS
CN Fluorosulfoxylic acid (9CI) (CA INDEX NAME)

F—S—OH

REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 13 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:344978 HCAPLUS
DOCUMENT NUMBER: 141:291969
TITLE: Reduction of Fe(III) (hydr)oxides with known thermodynamic stability by Geobacter metallireducens
AUTHOR(S): Dominik, Peter; Kaupenjohann, Martin
CORPORATE SOURCE: Institut fuer Bodenkunde und Standortslehre, Universitaet Hohenheim, Stuttgart, Germany
SOURCE: Geomicrobiology Journal (2004), 21(4), 287-295
CODEN: GEJODG; ISSN: 0149-0451
PUBLISHER: Taylor & Francis, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Sulfate-reducing and methanogenic microorganisms become inactive when the concentration of the electron donors drops below a threshold set by the min. Gibbs free energy required for the bacterial metabolism to be maintained. Thus, their activity is thermodynamically controlled. In this paper we study if the activity of dissimilatory Fe(III)-reducing bacteria is also limited by the thermodn. of the reaction. We synthesized five Fe(III) (hydr)oxides (**FHOs**) of moderate stability and determined the solubility product (log KSO (-39.1)-(-41.8)), in order to calculate their standard free energy of formation. KSO values, estimated from the particle size did not

correspond with exptl. determined ones. HCO3- and PIPES-buffered media, containing
45 mM FHO and either 1, 10, or 100 mM acetate, were inoculated with Geobacter metallireducens. At the end of bacterial reduction, the Gibbs free energy of the reaction showed significant differences between the different **FHOs**. The termination of the bacterial activity was consequently not triggered thermodynamically. However, the non-dissolved Fe(II) (HCl-soluble minus soluble Fe(II)) showed an excellent correlation with the surface of the **FHOs** (15 μmol m-2). It is therefore likely that the termination of the reaction was caused by blocking of the FHO surface with insol. Fe(II), as has been previously reported in the literature. The ecol. significance of both thermodn. limitation and surface availability limitation is discussed for **FHOs** of different KSO in environments with approx. neutral pH.

REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 14 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:312890 HCAPLUS
DOCUMENT NUMBER: 141:48234
TITLE: Identification and characterization of human FHOD3 gene in silico
AUTHOR(S): Katoh, Masuko; Katoh, Masaru
CORPORATE SOURCE: M+M Medical BioInformatics, Narashino, 275-0022, Japan
SOURCE: International Journal of Molecular Medicine (2004), 13(4), 615-620
CODEN: IJMMFG; ISSN: 1107-3756
PUBLISHER: International Journal of Molecular Medicine
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Formin homol. proteins are actin regulators with scaffold function, which are implicated in organogenesis, normal tissue homeostasis, and cancer-cell invasion. FHOD1/**FHOS**, GRID2IP, Fmn1 and Fmn2 are non-FDD-type Formin homol. proteins, while FMNL1, FMNL2/FHOD2, FMNL3, DAAM1, DAAM2, DIAPH1, DIAPH2 and DIAPH3 are FDD-type Formin homol. proteins. Here, we identified and characterized FHOD3 (also known as FHOS2), a novel gene homologous to FHOD1, by using bioinformatics. Because FLJ46173, FLJ22297, KIAA1695 and FLJ34580 were partial FHOD3 cDNAs, complete coding sequence of FHOD3 cDNA was determined by assembling nucleotide sequences of FLJ46173 and FLJ22297. FHOD3 gene at human chromosome 18q12.2 was found consisting of at least 25 exons. Exon 11 of FHOD3 gene was spliced out in KIAA1695 cDNA and BF116064 EST, while exon 13 of FHOD3 gene was spliced out in FLJ46173 cDNA. FHOD3 gene encodes at least three isoforms due to alternative splicing of the exon skipping type. FHOD3 and FHOD1 showed 52.1% total-amino-acid identity. Drosophila CG32030 showed 43.9% total-amino-acid identity with human FHOD3, and 39.1% total-amino-acid identity with human FHOD1. FHDHN domain (codon 1-327 of FHOD3) and FHDHC domain (codon 1377-1421 of FHOD3) were identified as the N-terminal conserved region and the juxta C-terminal conserved region, resp. Human FHOD3, FHOD1 and Drosophila CG32030 were found to share the conserved domain structure consisting of FHDHN, FH1, FH2, and FHDHC domains. This is the first report on the FHOD3 gene as well as on the novel FHDHN and FHDHC domains.

REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 15 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:952207 HCAPLUS
DOCUMENT NUMBER: 140:108802
TITLE: **Fhos**, a mammalian formin, directly binds to

F-actin via a region N-terminal to the FH1 domain and forms a homotypic complex via the FH2 domain to promote actin fiber formation
AUTHOR(S): Takeya, Ryu; Sumimoto, Hideki
CORPORATE SOURCE: Medical Institute of Bioregulation, Kyushu University, Fukuoka, 812-8582, Japan
SOURCE: Journal of Cell Science (2003), 116(22), 4567-4575
CODEN: JNCSAI; ISSN: 0021-9533
PUBLISHER: Company of Biologists Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Formins constitute a family of eukaryotic proteins that are considered to function as a cytoskeleton organizer to regulate morphogenesis, cell polarity and cytokinesis. **Fhos** is a recently identified mammalian formin, which contains the conserved domains FH (formin homol.) 1 and FH2 in the middle region and the Dia-autoregulatory domain (DAD) in the C-terminus. The role of **Fhos** in the regulation of cytoskeleton, however, has remained unknown. Here we show that **Fhos**, in an active form, induces the formation of actin stress fibers and localizes to the actin-based structure. **Fhos** appears to normally exist in a closed inactive form via an intramol. interaction between the N-terminal region and the C-terminal DAD. Both FH1 and FH2 domains are required for the induction of the stress fiber formation. However, the N-terminal region of **Fhos** is required for the targeting of this protein to stress fibers, which is probably mediated via its F-actin-binding activity. We also show that **Fhos** occurs as a homotypic complex in cells. The self-association of **Fhos** seems to be mediated via the FH2 domain: the domains bind to each other in a direct manner. Thus, the mammalian formin **Fhos**, which directly binds to F-actin via the N-terminal region, forms a homotypic complex via the FH2 domain to organize actin cytoskeleton.
REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 16 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:526882 HCAPLUS
DOCUMENT NUMBER: 139:289626
TITLE: The formin family protein, formin homolog overexpressed in spleen, interacts with the insulin-responsive aminopeptidase and profilin IIa
AUTHOR(S): Tojo, Hideaki; Kaieda, Isao; Hattori, Harumi; Katayama, Nozomi; Yoshimura, Koji; Kakimoto, Shigeya; Fujisawa, Yukio; Presman, Eleonora; Brooks, Cydney C.; Pilch, Paul F.
CORPORATE SOURCE: Discovery Research Laboratories II, Pharmaceutical Research Division, Takeda Chemical Industries Co., Ltd., Ibaraki, 300-4293, Japan
SOURCE: Molecular Endocrinology (2003), 17(7), 1216-1229
CODEN: MOENEN; ISSN: 0888-8809
PUBLISHER: Endocrine Society
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Insulin stimulates translocation of glucose transporter isoform type 4 (GLUT4) and the insulin-responsive aminopeptidase (IRAP) from an intracellular storage pool to the plasma membrane in muscle and fat cells. A role for the cytoskeleton in insulin action has been postulated, and the insulin signaling pathway has been well investigated; however, the mol. mechanism by which GLUT4/IRAP-containing vesicles move from an interior location to the cell surface in response to insulin is incompletely understood. Here, we have screened for IRAP-binding proteins using a

yeast two-hybrid system and have found that the C-terminal domain of **FHOS** (formin homolog overexpressed in spleen) interacts with the N-terminal cytoplasmic domain of IRAP. **FHOS** is a member of the Formin/Diaphanous family of proteins that is expressed most abundantly in skeletal muscle. In addition, there are two novel types of **FHOS** transcripts generated by alternative mRNA splicing. FHOS78 has a 78-bp insertion and it is expressed mainly in skeletal muscle where it may be the most abundant isoform in humans. The ubiquitously expressed FHOS24 has a 24-bp insertion encoding an in-frame stop codon that results in a truncated polypeptide. It is known that some formin family proteins interact with the actin-binding profilin proteins. Both **FHOS** and FHOS78 bound to profilin IIa via their formin homol. 1 domains, but neither bound profilin I or IIb. Overexpression of **FHOS** and FHOS78 resulted in enhanced insulin-stimulated glucose uptake in L6 cells to similar levels. However, overexpression of FHOS24, lacking the IRAP-binding domain, did not affect insulin-stimulated glucose uptake. These findings suggest that **FHOS** mediates an interaction between GLUT4/IRAP-containing vesicles and the cytoskeleton and may participate in exocytosis and/or retention of this membrane compartment.

IT **607747-80-8**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; interaction of **FHOS** (formin homolog overexpressed in spleen) with insulin-responsive aminopeptidase (IRAP) and profilin IIa and effects on insulin-stimulated glucose uptake by muscle)

RN 607747-80-8 HCAPLUS
CN Protein FHOS (formin homolog overexpressed in spleen) (human muscle-specific isoform FHOS78) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 42 THERE ARE 42 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 17 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:555526 HCAPLUS
DOCUMENT NUMBER: 137:121351
TITLE: Interactions between proteins of Shigella flexneri and mammals playing a role in the pathogenesis of shigellosis for development of therapeutics
INVENTOR(S): Legrain, Pierre
PATENT ASSIGNEE(S): Hybrigenics, Fr.
SOURCE: PCT Int. Appl., 162 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002057303	A2	20020725	WO 2002-EP777	20020111
WO 2002057303	A3	20031224		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY,

KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003055220 A1 20030320 US 2002-43487 20020111
PRIORITY APPLN. INFO.: US 2001-261130P P 20010112

AB The present invention relates to protein-protein interactions between proteins of Shigella and their mammalian hosts that may play a role in the pathogenesis of shigellosis and may therefore be of use in the development of therapeutic agents. More specifically, the present invention relates to complexes of polypeptides or polynucleotides encoding the polypeptides, fragments of the polypeptides, antibodies, to the complexes, Selected Interacting Domains (SID) which are identified due to the protein-protein interactions, methods for screening drugs for agents which modulate the interaction of proteins and pharmaceutical composition that are capable of modulating the protein-protein interactions. Proteins of human placenta that interact with proteins of Shigella flexneri were identified by two-hybrid screening.

IT **444205-90-7**, Protein **FHOS** (human clone prey3297)
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; interactions between proteins of Shigella flexneri and mammals in pathogenesis of shigellosis and development of therapeutics)
RN 444205-90-7 HCAPLUS
CN Protein FHOS (human clone prey3297) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **444125-02-4**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; interactions between proteins of Shigella flexneri and mammals in pathogenesis of shigellosis and development of therapeutics)
RN 444125-02-4 HCAPLUS
CN DNA (human clone prey3296 protein FHOS-specifying) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 18 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:521969 HCAPLUS
DOCUMENT NUMBER: 137:90000
TITLE: Protein-protein interactions in adipocyte cells and method for selecting modulators of these interactions
INVENTOR(S): Legrain, Pierre; Marullo, Stefano; Jockers, Ralf
PATENT ASSIGNEE(S): Hybrigenics, Fr.; Centre National De La Recherche Scientifique
SOURCE: PCT Int. Appl., 125 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002053726	A2	20020711	WO 2001-EP15423	20011228
WO 2002053726	A3	20030313		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,

LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,
UG, US, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR,
BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2003040089	A1	20030227	US 2002-38010	20020102
PRIORITY APPLN. INFO.:			US 2001-259377P	P 20010102

AB The present invention relates to protein-protein interactions of adipocyte. More specifically, the present invention relates to complexes of polypeptides, or polynucleotides encoding the polypeptides, fragments of the polypeptides, antibodies to the complexes. Selected Interacting Domains (SID) which are identified due to the protein-protein interactions, methods for screening drugs for agents which modulate the interaction of proteins, and pharmaceutical compns. that are capable of modulating the protein-protein interactions are further disclosed.

L2 ANSWER 19 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:353605 HCAPLUS
DOCUMENT NUMBER: 136:364861
TITLE: Protein complexes playing a role in the etiology of metabolic diseases and their identification and use in the development of therapeutics
INVENTOR(S): Eisen, Andrew J.; Giot, Loic; Lewin, David A.
PATENT ASSIGNEE(S): Curagen Corporation, USA
SOURCE: PCT Int. Appl., 111 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002036766	A2	20020510	WO 2001-US48162	20011030
WO 2002036766	A3	20030710		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH,
GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,
LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH,
PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA,
UG, US, UZ, VN, YU, ZA, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AM, AZ, BY, KG,
KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR,
IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN,
GQ, GW, ML, MR, NE, SN, TD, TG

AU 2002029037	A5	20020515	AU 2002-29037	20011030
US 2003157554	A1	20030821	US 2001-4083	20011030
PRIORITY APPLN. INFO.:			US 2000-244236P	P 20001030
			WO 2001-US48162	W 20011030

AB Protein complexes of proteins involved in the etiol. of metabolic disease including obesity and diabetes are identified for use. The complexes, which may involve fusion proteins of the binding partners with reporter moieties, may be used to screen for effectors of the interaction, or to determine levels of the complex in a patient and to monitor the effectiveness of treatment. Sequences of cDNAs of novel proteins involved in these interactions are also reported.

L2 ANSWER 20 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:908589 HCAPLUS

DOCUMENT NUMBER: 136:181029
TITLE: The formin/diaphanous-related protein, **FHOS**, interacts with Rac1 and activates transcription from the serum response element
AUTHOR(S): Westendorf, Jennifer J.
CORPORATE SOURCE: Department of Orthopaedic Surgery and University of Minnesota Cancer Center, University of Minnesota, Minneapolis, MN, 55455, USA
SOURCE: Journal of Biological Chemistry (2001), 276(49), 46453-46459
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB **FHOS** is a member of the formin homol. (FH) family of proteins and is expressed at high levels in splenic cells. FH proteins link cellular signaling pathways to the actin cytoskeleton and serum response factor-dependent transcription. In these studies, the role of **FHOS** in Rho family GTPase signaling pathways was analyzed. **FHOS** interacted with the polybasic domain in the Rac1 C terminus in a guanine nucleotide-independent manner but did not interact with RhoA, Cdc42Hs, Rac2, or Rac3. Intramol. autoinhibitory interactions between the C terminus of **FHOS** and an N-terminal region partially overlapping the Rac1 interaction domain were also identified. **FHOS** truncation mutants lacking the N- or C-terminal autoregulatory domains stimulated transcription of a c-fos serum response element (SRE)-driven reporter. Overexpression of wild-type and mutant (N17 and V12) Rac1 proteins repressed SRE induction by the N-terminal **FHOS** deletion mutant but not by the C-terminal **FHOS** deletion mutant. Immunofluorescence studies indicated that the localization of the mutant **FHOS** proteins might contribute to their differential responses to Rac1. Wild-type **FHOS** and the N-terminal deletion mutant localized to the perinuclear region and membrane edges. In contrast, the C-terminal **FHOS** mutants were diffusely localized. These data suggest that **FHOS** induces transcription from SREs by multiple pathways and that Rac1 may influence the course of some **FHOS**-induced signaling events.
REFERENCE COUNT: 47 THERE ARE 47 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:890709 HCAPLUS
DOCUMENT NUMBER: 136:63023
TITLE: On fluoride sulfides (MFS) of the lanthanides (M = La-Nd, Sm, Gd-Lu) with A- or PbFCl-type crystal structure
AUTHOR(S): Schleid, Thomas; Grossholz, Hagen
CORPORATE SOURCE: Institut fur Anorganische Chemie, Universitat Stuttgart, Stuttgart, D-70569, Germany
SOURCE: Zeitschrift fuer Anorganische und Allgemeine Chemie (2001), 627(12), 2693-2699
CODEN: ZAACAB; ISSN: 0044-2313
PUBLISHER: Wiley-VCH Verlag GmbH
DOCUMENT TYPE: Journal
LANGUAGE: German
AB By the reaction of the elemental lanthanides (M = La-nd, Sm-Lu) with the resp. trifluorides (MF3) and S in 2:1:3-molar ratios at 850°, single-phase fluoride sulfides of the composition MFS can be obtained in evacuated, gas-tightly arc-welded Nb or Ta capsules within a few days.

Exceptions are Eu and Yb which do not react to form the corresponding fluoride sulfides under these conditions. However, at least YbFS becomes accessible through this method if Pt serves as container material. With NaCl as a flux, the formation of hydrolysis-insensitive, platelet-shaped A-type single crystals with square cross-section and the formula MFS (M = La-Nd, Sm, Gd-Er) is possible. These are very suitable for structure refinement from x-ray diffraction data. In the PbFCl-analogous crystal structures (tetragonal, P4/nmm, Z = 2; LaFS: a = 404.38(4), c = 700.41(7) pm; CeFS: a = 400.13(3), c = 606.20(5) pm; PrFS: a = 396.27(3), c = 692.72(5) pm; NdFS: a = 393.89(3), c = 691.58(5) pm; SmFS: a = 388.36(3), c = 687.95(5) pm; GDFS: a = 383.45(3), c = 685.18(5) pm; TBFS: a = 381.02(3), c = 683.86(5) pm; DyFS: a = 378.48(2), c = 682.51(4) pm; HoFS: a = 376.48(3), c = 681.92(5) pm; ErFS: a = 374.61(3), c = 681.34(5) pm), the M3+ cations are surrounded by 9 anions (4F- and 5S2-) as monocapped square antiprisms. The anions themselves exhibit tetrahedral (F-) and square-pyramidal (S2-) cationic coordination, resp., according to the Niggli formula $3\infty\{(M3+)(F-)4/4(S2-)5/5\}$. In the case of TmFS, YbFS, and LuFS under analogous conditions, the hexagonal B- or trigonal C-type modifications form at first, which can be transformed eventually to th quenchable metastable tetragonal A-type polymorphs (TmFS: a = 372.86(5), c = 681.15(8) pm; YbFS: a = 371.08(5), c = 680.93(8) pm; LuFS: a = 369.37(5), c = 680.76(8) pm) at high pressure (20-60 kbar).

IT **25180-88-5P**, Holmium fluoride sulfide (HoFS)
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(preparation, crystal structure, and Madelung lattice energy of)

RN 25180-88-5 HCAPLUS

CN Holmium fluoride sulfide (HoFS) (8CI, 9CI) (CA INDEX NAME)

F—Ho═S

REFERENCE COUNT: 58 THERE ARE 58 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:785622 HCAPLUS
DOCUMENT NUMBER: 135:314495
TITLE: Differentially expressed nucleic acids encoding tumor-associated proteins, kits, and methods for identification, assessment, prevention, and therapy of human prostate cancer
INVENTOR(S): Schlegel, Robert; Endege, Wilson; Monahan, John E.
PATENT ASSIGNEE(S): Millennium Predictive Medicine, Inc., USA
SOURCE: PCT Int. Appl., 975 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001053836	A2	20010726	WO 2001-XC2318	20010124

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

WO 2001053836 A2 20010726 WO 2001-US2318 20010124
WO 2001053836 A3 20020606
WO 2001053836 C2 20021107

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN,
CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR,
HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT,
LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU,
SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU,
ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY,
DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF,
BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 2000-178525P P 20000124
US 2000-183245P P 20000217
US 2000-190139P P 20000316
US 2000-208126P P 20000531
US 2000-219705P P 20000718
US 2000-255160P P 20001213
WO 2001-US2318 A 20010124

AB This invention relates to newly discovered correlations between expression of certain nucleic acid markers and the cancerous state of human prostate cells. The levels of expression of individual markers and combinations of markers described herein correlates with the presence of prostate cancer or a pre-malignant condition in a patient. Methods are provided for detecting the presence of prostate cancer in a sample, the absence of prostate cancer in a sample, the stage of a prostate cancer, the metastatic potential of a prostate cancer, the indolence or aggressiveness of the cancer, and other characteristics of prostate cancer that are relevant to prevention, diagnosis, characterization and therapy of prostate cancer in a patient. Thousands of differentially-expressed cDNA markers are identified in subtracted cDNA libraries and by transcript profiling. [This abstract record is the fourth of four records for this document necessitated by the large number of index entries required to fully index the document and publication system constraints.].

IT **226205-37-4**
RL: ANT (Analyte); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; differentially expressed nucleic acids encoding tumor-associated proteins, kits, and methods for identification, assessment, prevention, and therapy of human prostate cancer)

RN 226205-37-4 HCAPLUS
CN DNA (human gene FHOS NLS FH1/FH2 domain-containing protein cDNA) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L2 ANSWER 23 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2001:472920 HCAPLUS
DOCUMENT NUMBER: 135:87999
TITLE: cDNAs for insulin-responsive aminopeptidase and glucose transporter 4 binding proteins MD36 and **FHOS**, from human and mouse, and uses in diagnostic, therapeutic, and drug screening applications
INVENTOR(S): Tojo, Hideaki; Katayama, Nozomi; Kakimoto, Shigeya

PATENT ASSIGNEE(S): Takeda Chemical Industries, Ltd., Japan
SOURCE: PCT Int. Appl., 186 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001046413	A1	20010628	WO 2000-JP8985	20001219
W: AE, AG, AL, AM, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CN, CR, CU, CZ, DM, DZ, EE, GD, GE, HR, HU, ID, IL, IN, IS, JP, KG, KR, KZ, LC, LK, LR, LT, LV, MA, MD, MG, MK, MN, MX, NO, NZ, PL, RO, RU, SG, SI, SK, TJ, TM, TR, TT, UA, US, UZ, VN, YU, ZA, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
CA 2394757	AA	20010628	CA 2000-2394757	20001219
AU 2001018946	A5	20010703	AU 2001-18946	20001219
JP 2001238685	A2	20010904	JP 2000-385386	20001219
EP 1241256	A1	20020918	EP 2000-981825	20001219
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
US 2004072742	A1	20040415	US 2002-168067	20020614

PRIORITY APPLN. INFO.:
JP 1999-361679 A 19991220
JP 1999-365176 A 19991222
WO 2000-JP8985 W 20001219

AB The invention provides cDNA sequences encoding human and mouse proteins MD36 and **FHOS** which binds to IRAP (insulin-responsive aminopeptidase) and GLUT4 (glucose transporter 4) (IRAP-BP). Since IRAP is involved in regulating insulin-responsive translocation of the glucose transporter GLUT4, IRAP-BP also has a role in insulin-sensitive cellular responses. The invention further provides recombinant expression of those proteins, and antibodies. Diagnostic reagents and kits, and drug screening for therapeutic agents for diseases such as hyperglycemia and diabetes are also provided. Screening of 2 compds. that inhibited MD36 binding to IRAP and binding of MD36 to profilin IIL, are described.

IT **244251-72-7P**
RL: ARU (Analytical role, unclassified); BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); ANST (Analytical study); BIOL (Biological study); OCCU (Occurrence); PREP (Preparation); USES (Uses)
(amino acid sequence; cDNAs for insulin-responsive aminopeptidase and glucose transporter 4 binding proteins MD36 and **FHOS**, from human and mouse, and uses in diagnostic, therapeutic, and drug screening applications)
RN 244251-72-7 HCAPLUS
CN FH1/FH2 domain-containing protein FHOS (human gene FHOS) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***
REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 24 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1999:436014 HCAPLUS
DOCUMENT NUMBER: 131:239309

TITLE: Identification and characterization of a protein containing formin homology (FH1/FH2) domains
AUTHOR(S): Westendorf, Jennifer J.; Mernaugh, Ray; Hiebert, Scott W.
CORPORATE SOURCE: Vanderbilt Cancer Center, Department of Biochemistry, Vanderbilt University, Nashville, TN, USA
SOURCE: Gene (1999), 232(2), 173-182
CODEN: GENED6; ISSN: 0378-1119
PUBLISHER: Elsevier Science B.V.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB A novel member of the Formin/Diaphanous family of proteins was cloned and characterized. A 4 kB mRNA is ubiquitously expressed but is found in abundance in the spleen. **FHOS** (Formin Homolog Overexpressed in Spleen) contains a 3414 bp open reading frame and encodes for an approx. 128 kDa protein. **FHOS** has sequence homol. to Diaphanous and Formin proteins within the Formin Homol. (FH)1 and FH2 domains. **FHOS** also contains a coiled-coil, a collagen-like domain, two nuclear localization signals, and several potential PKC and PKA phosphorylation sites. **FHOS**-specific antiserum was generated and used to determine that **FHOS** is a predominantly cytoplasmic protein and is expressed in a variety of human cell lines. **FHOS** was mapped to chromosome 16q22 between framework markers WI-5594 and WI-9392.

IT **244251-72-7**
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; identification and characterization of protein containing formin homol. (FH1/FH2) domains)
RN 244251-72-7 HCAPLUS
CN FH1/FH2 domain-containing protein FHOS (human gene FHOS) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **226205-37-4**, GenBank AF113615
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; identification and characterization of protein containing formin homol. (FH1/FH2) domains)
RN 226205-37-4 HCAPLUS
CN DNA (human gene FHOS NLS FH1/FH2 domain-containing protein cDNA) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

REFERENCE COUNT: 28 THERE ARE 28 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 25 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1997:700408 HCAPLUS
DOCUMENT NUMBER: 128:7544
TITLE: A study of sulfur-containing molecules using Hartree-Fock, MP2, and DFT (hybrid) methodologies
AUTHOR(S): Altmann, Julianna A.; Handy, Nicholas C.; Ingamells, Victoria E.
CORPORATE SOURCE: University of London Computer Centre, London, WC1N 1DZ, UK
SOURCE: Molecular Physics (1997), 92(3), 339-352
CODEN: MOPHAM; ISSN: 0026-8976
PUBLISHER: Taylor & Francis
DOCUMENT TYPE: Journal

LANGUAGE: English

AB The performance is examined of the B3P86 hybrid exchange-correlation function for a set of 21 sulfur-containing mols. Optimized geometries, harmonic frequencies, and mean mol. polarizabilities are presented, and compared with calcns. to the Hartree-Fock and MP2 levels of theory, and with appropriate exptl. results. The hybrid functional predicts geometries at a level comparable with the MP2 results; harmonic frequencies are in closer agreement with exptl. results than either MP2 or Hartree-Fock method; mean mol. polarizabilities predicted by the hybrid functional appear to be substantially closer to experiment than those calculated by either of the other two methods.

IT **83045-12-9**, Fluorosulfoxylic acid
RL: PRP (Properties)
(mol. structures, mol. vibrations, and polarizabilities of sulfur-containing mols. studied by using Hartree-Fock, MP2, and DFT (hybrid) methodologies)

RN 83045-12-9 HCAPLUS

CN Fluorosulfoxylic acid (9CI) (CA INDEX NAME)

F—S—OH

REFERENCE COUNT: 54 THERE ARE 54 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 26 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1988:637409 HCAPLUS

DOCUMENT NUMBER: 109:237409

TITLE: The use of theoretical indexes for the characterization of sulfur-oxygen linkage multiplicity

AUTHOR(S): Angyan, J. G.; Bonnelle, C.; Daudel, R.; Kucsman, A.; Csizmadia, I. G.

CORPORATE SOURCE: Lab. Chim. Phys., Univ. Pierre et Marie Curie, Paris, 75005, Fr.

SOURCE: THEOCHEM (1988), 42(3-4), 273-87
CODEN: THEODJ; ISSN: 0166-1280

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The nature and strength of S-O bonding was investigated by ab initio theor. calcns. on a series of sulfenic acids, sulfoxides, sulfones, and sulfuranes. The S-O bond orders and the valence of S were computed at fully optimized geometries with STO-3G, STO-3G*, and 3-21G* basis sets, and were correlated with the calculated S-O bond lengths and S 2p ionization potentials, resp. The S-O linkage was characterized by several exptl. and theor. indexes in a wide range of bond lengths. Further evidence was found to support the importance of the sulfur d-orbitals in hypervalent compds.

IT **83045-12-9**, Fluorosulfoxylic acid
RL: PRP (Properties)
(oxygen-sulfur bonding and sulfur valence in, ab-initio calcns. on)

RN 83045-12-9 HCAPLUS

CN Fluorosulfoxylic acid (9CI) (CA INDEX NAME)

F—S—OH

L2 ANSWER 27 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1984:464848 HCAPLUS
DOCUMENT NUMBER: 101:64848
TITLE: Precision lattice constants of the rare earth sulfofluorides of the type LnSF
AUTHOR(S): Brixner, L.; Hyatt, G.
CORPORATE SOURCE: Cent. Res. Dev. Dep., E. I. du Pont de Nemours and Co., Wilmington, DE, 19898, USA
SOURCE: Materials Research Bulletin (1984), 19(6), 745-50
CODEN: MRBUAC; ISSN: 0025-5408
DOCUMENT TYPE: Journal
LANGUAGE: English
AB LnSF (Ln = Y, La-Lu except Pm) were prepared by the interaction of H2S and LnF3 at 900-1000°. Only EuSF could not be prepared this way and the new EuS0.5F was obtained. Using this technique, LnSF (Ln = La-Ho) are tetragonal, space group P4/nmm, whereas LnSF (Ln = Er-Lu) are hexagonal, space group P6322. Refined cell consts. of all compds. are reported.
IT **25180-88-5P**
RL: PRP (Properties); SPN (Synthetic preparation); PREP (Preparation)
(preparation and crystal structure of)
RN 25180-88-5 HCAPLUS
CN Holmium fluoride sulfide (HoFS) (8CI, 9CI) (CA INDEX NAME)

F—Ho═S

L2 ANSWER 28 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1972:494032 HCAPLUS
DOCUMENT NUMBER: 77:94032
TITLE: Crystal chemical study of samarium group rare earth sulfidofluorides
AUTHOR(S): Filatkina, V. S.; Kustova, G. N.
CORPORATE SOURCE: Inst. Katal., Novosibirsk, USSR
SOURCE: Izvestiya Akademii Nauk SSSR, Seriya Khimicheskaya (1972), (6), 1254-7
CODEN: IASKA6; ISSN: 0002-3353
DOCUMENT TYPE: Journal
LANGUAGE: Russian
AB The sulfidofluorides were prepared by heating stoichiometric mixts. of components at 900° 6 hr in evacuated quartz capsules containing Pt crucibles. The resulting SmSF, GdSF, DySF, HoSF, and ErSF are described. The 1st 3 crystallize similarly to PbFCl; the remainder do not belong to this type. The unit-cell parameters and interat. distances were calculated for the 1st 3 compds., and ir spectra are shown and discussed.
IT **25180-88-5**
RL: PRP (Properties)
(crystal structure and ir spectrum of)
RN 25180-88-5 HCAPLUS
CN Holmium fluoride sulfide (HoFS) (8CI, 9CI) (CA INDEX NAME)

F—Ho═S

L2 ANSWER 29 OF 29 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1969:475188 HCAPLUS
DOCUMENT NUMBER: 71:75188

TITLE: Distribution of crystal types in series of iodosulfides and fluorosulfides of rare earth elements and yttrium
AUTHOR(S): Dagron, Christian; Thevet, Francoise
CORPORATE SOURCE: Fac. Pharm. Paris, Paris, Fr.
SOURCE: Comptes Rendus des Seances de l'Academie des Sciences, Serie C: Sciences Chimiques (1969), 268(21), 1867-9
CODEN: CHDCAQ; ISSN: 0567-6541
DOCUMENT TYPE: Journal
LANGUAGE: French
AB Three types of crystals are demonstrated for the iodosulfides of rare-earth elements: orthorhombic, space group Pcab, for LaSI and α-CeSI; monoclinic, space group B2/m, from CeSI to SmSI; hexagonal from GdSI to LuSI. The fluorosulfides are divided in 2 series: tetragonal PbClF type from LaSF to α-HoSF, α-ErSF, and αYSF; hexagonal, space group P6322 for β-HoSF, β-ErSF, YbSF, LuSF, and β-YSF. Dimensions of each of the unit cells are given.
IT **25180-88-5**
RL: PRP (Properties)
(crystal structure of)
RN 25180-88-5 HCAPLUS
CN Holmium fluoride sulfide (HoFS) (8CI, 9CI) (CA INDEX NAME)

F—Ho═S

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L1 95 SEA FILE=REGISTRY ABB=ON PLU=ON FHOS/BI
L2 29 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 OR FHOS
L3 259 SEA FILE=REGISTRY ABB=ON PLU=ON FORMIN/BI
L4 44779 SEA FILE=HCAPLUS ABB=ON PLU=ON L3 OR FORMIN
L5 1163 SEA FILE=HCAPLUS ABB=ON PLU=ON L4(L)(?DIABET? OR INSULIN(2A)RESIS? OR ?GLYCEM?)
L6 796 SEA FILE=HCAPLUS ABB=ON PLU=ON L4(L)(MRNA OR DNA OR ?NUCLE? OR PROTEIN)
L7 25 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 AND L5
L8 24 SEA FILE=HCAPLUS ABB=ON PLU=ON L7 NOT L2

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L8 ANSWER 1 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:458000 HCAPLUS
DOCUMENT NUMBER: 143:298845
TITLE: Effect of sodium orthovanadate on GLUT4 mRNA expression in the skeletal muscle of type 2 diabetic rats
AUTHOR(S): Wang, Ning; Ai, Jing; Yang, Mei; Fang, Zhiwei; Du, Zhimin; Yang, Baofeng
CORPORATE SOURCE: Department of Pharmacology, Harbin Medical University, Harbin, Heilongjiang Province, 150086, Peop. Rep. China
SOURCE: Zhongguo Yaoxue Zazhi (Beijing, China) (2004), 39(11), 828-830
CODEN: ZYZAEU; ISSN: 1001-2494
PUBLISHER: Zhongguo Yaoxue Zazhishe
DOCUMENT TYPE: Journal

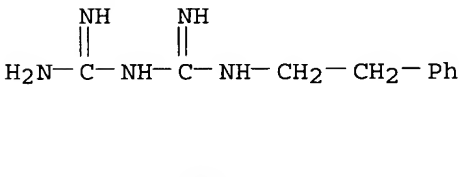
LANGUAGE: Chinese

AB The rats were feed with high-fat food for 10 days to get obese. The rats with plasma glucose levels higher than 16.7 mmol·L-1 were selected, and organized into 5 groups randomly: sodium orthovanadate high dose group (9 mg·kg-1·d-1), middle dose group (3 mg·kg-1·d-1), low dose group (1 mg·kg-1·d-1), diabetes model group, and meltrol group (75 mg·kg-1·d-1).Alloxan (120 mg·kg-1) was given to the rts by i.p., establishing type 2 diabetes model. The rats with plasma glucose levels higher than 16.7 mmol·L-1 were selected, and organized into 5 groups randomly: sodium orthovanadate high dose group (9 mg·kg-1·d-1), middle dose group (3 mg·kg-1·d-1), low dose group (1 mg·kg-1·d-1), diabetes model group, and meltrol group (75 mg·kg-1·d-1). The rats in sodium orthovanadate groups were administered for 7 days, and then the levels of plasma glucose and insulin were assayed. Glucose transporter 4 (GLUT4) mRNA expression in the skeletal muscle was determined by the hybridization in situ technique. After fed with sodium orthovanadate, the plasma glucose levels of the type 2 diabetic rats were obviously lower than those of the diabetes model rats ($P<0.05$). There was no obvious difference for the plasma insulin value between the sodium orthovanadate group and the diabetes model rats. GLUT4 mRNA expression in the skeletal muscle of the diabetic rats fed with sodium orthovanadate was obviously greater than that of the diabetes model rats. The study suggested that sodium orthovanadate can decrease plasma glucose level, and promote GLUT4 mRNA expression in the skeletal muscle of the type 2 diabetic rats.

IT **834-28-6**, Meltrol
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(effect of sodium orthovanadate on GLUT4 **mRNA** expression in the skeletal muscle of type 2 **diabetic** rats)

RN 834-28-6 HCAPLUS

CN Imidodicarbonimidic diamide, N-(2-phenylethyl)-, monohydrochloride (9CI) (CA INDEX NAME)



● HCl

L8 ANSWER 2 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2004:1088101 HCAPLUS

DOCUMENT NUMBER: 143:4824

TITLE: Up-regulation of PPARγ coactivator-1α as a strategy for preventing and reversing insulin resistance and obesity

AUTHOR(S): McCarty, Mark F.

CORPORATE SOURCE: NutriGuard Research, Encinitas, CA, 92024, USA

SOURCE: Medical Hypotheses (2005), 64(2), 399-407
CODEN: MEHYDY; ISSN: 0306-9877

PUBLISHER: Elsevier Ltd.

DOCUMENT TYPE: Journal; General Review

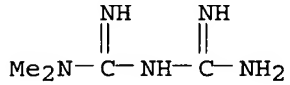
LANGUAGE: English

AB A review. Excessive accumulation of triglycerides and certain fatty acid

derivs. in skeletal muscle and other tissues appears to mediate many of the adverse effects of insulin resistance syndrome. Although fatty diets and obesity can promote such accumulation, deficient capacity for fatty acid oxidation can also contribute in this regard. Indeed, in subjects who are insulin resistant, diabetic, and/or obese, fatty acid oxidation by skeletal muscle tends to be inefficient, reflecting decreased expression of mitochondria and mitochondrial enzymes in muscle. This phenomenon is not corrected by weight loss, is not simply reflective of subnormal phys. activity, and is also seen in lean first-degree relatives of diabetics; thus, it appears to be primarily attributable to genetic factors. Recent studies indicate that decreased expression of PPARγ coactivator-1α (PGC-1α), a "master switch" which induces mitochondrial biogenesis by supporting the transcriptional activity of the nuclear respiratory factors, may largely account for the diminished oxidative capacity of subjects prone to insulin resistance. Thus, feasible measures which up-regulate PGC-1α may be useful for preventing and treating insulin resistance and obesity. These may include exercise training, metformin and other agents which stimulate AMP-activated kinase, high-dose biotin, and PPARδ agonists. Drugs which are specific agonists for PPARδ show remarkable efficacy in rodent models of insulin resistance, diabetes, and obesity, and are currently being evaluated clin. Phytanic acid, a branched-chain fatty acid found in omnivore diets, can also activate PPARδ, and thus should be examined with respect to its impact on mitochondrial biogenesis and insulin sensitivity.

IT **657-24-9**, Metformin
RL: BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(metformin, high-dose biotin, PPARδ agonist up-regulate of PGC-1α is effective, induced mitochondrial biogenesis by activation of **nuclear** respiratory factor which is useful in treating **insulin resistance**, **diabetes**, obesity in mouse model)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 114 THERE ARE 114 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

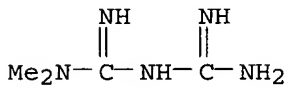
L8 ANSWER 3 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:939417 HCAPLUS
DOCUMENT NUMBER: 142:536
TITLE: AMP-activated Protein Kinase is Required for the Lipid-lowering Effect of Metformin in Insulin-resistant Human HepG2 Cells
AUTHOR(S): Zang, Mengwei; Zuccollo, Adriana; Hou, Xiuyun; Nagata, Daisuke; Walsh, Kenneth; Herscovitz, Haya; Brecher, Peter; Ruderman, Neil B.; Cohen, Richard A.
CORPORATE SOURCE: Vascular Biology Unit, Boston University School of Medicine, Boston, MA, 02118, USA
SOURCE: Journal of Biological Chemistry (2004), 279(46), 47898-47905
CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The antidiabetic drug metformin stimulates AMP-activated protein kinase (AMPK) activity in the liver and in skeletal muscle. To better understand the role of AMPK in the regulation of hepatic lipids, we studied the effect of metformin on AMPK and its downstream effector, acetyl-CoA carboxylase (ACC), as well as on lipid content in cultured human hepatoma HepG2 cells. Metformin increased Thr-172 phosphorylation of the α subunit of AMPK in a dose- and time-dependent manner. In parallel, phosphorylation of ACC at Ser-79 was increased, which was consistent with decreasing ACC activity. Intracellular triacylglycerol and cholesterol contents were also decreased. These effects of metformin were mimicked or completely abrogated by adenoviral-mediated expression of a constitutively active AMPKα or a kinase-inactive AMPKα, resp. An insulin-resistant state was induced by exposing cells to 30 mM glucose as indicated by decreased phosphorylation of Akt and its downstream effector, glycogen synthase kinase 3α/β. Under these conditions, the phosphorylation of AMPK and ACC was also decreased, and the level of hepatocellular triacylglycerols increased. The inhibition of AMPK and the accumulation of lipids caused by high glucose concns. were prevented either by metformin or by expressing the constitutively active AMPKα. The kinase-inactive AMPKα increased lipid content and blocked the ability of metformin to decrease lipid accumulation caused by high glucose concns. Taken together, these results indicate that AMPKα neg. regulates ACC activity and hepatic lipid content. Inhibition of AMPK may contribute to lipid accumulation induced by high concns. of glucose associated with insulin resistance. Metformin lowers hepatic lipid content by activating AMPK, thereby mediating beneficial effects in hyperglycemia and insulin resistance.

IT **657-24-9**, Metformin
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(AMP-activated **protein** kinase is required for the lipid-lowering effect of metformin in **insulin-resistant** human HepG2 cells)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 49 THERE ARE 49 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

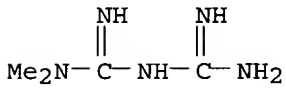
L8 ANSWER 4 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:886814 HCAPLUS
DOCUMENT NUMBER: 141:393224
TITLE: Adiponectin and C-reactive protein in obesity, type 2 diabetes, and monodrug therapy
AUTHOR(S): Putz, Darcy M.; Goldner, Whitney S.; Bar, Robert S.; Haynes, William G.; Sivitz, William I.
CORPORATE SOURCE: Iowa City Veterans Affairs Medical Center, Department of Internal Medicine, Division of Endocrinology and Metabolism, The University of Iowa, Iowa City, IA, USA
SOURCE: Metabolism, Clinical and Experimental (2004), 53(11),

1454-1461
CODEN: METAAJ; ISSN: 0026-0495
PUBLISHER: Elsevier Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB To learn more about the factors that regulate adipokines in diabetes, we examined fasting plasma concns. of adiponectin and C-reactive protein (CRP) in well-characterized groups of age-matched individuals classified as: (1) type 2 diabetes; (2) impaired fasting glucose or mild diabetes (IFG/mild DM); (3) obese, matched for body mass index (BMI); and (4) non-obese. Diabetic subjects were also studied on no phamacol. treatment, after 3 mo randomization to metformin or glyburide, and after 3 mo crossover to the opposite drug. CRP decreased and adiponectin increased progressively between subjects in groups 1 through 4. CRP was significantly associated with percent (r = 0.45) and total (r = 0.50) fat, insulin sensitivity as SI (r = -0.39) or homeostasis model assessment of insulin resistance [HOMA (IR)] (r = -0.36), and Hb A1c (HbA1c) (r = 0.41). The relationship of CRP to percent fat appeared to be logarithmic and log CRP varied with percent fat independent of gender. Adiponectin concentration was significantly associated with insulin sensitivity as SI (r = 0.55) or HOMA (IR) (r = -0.46). Adiponectin concns. were higher among women overall (all groups included) but not in women classified as type 2 diabetes. Although mean adiponectin was higher in subjects classified as non-obese compared to obese, adiponectin, in sharp contrast to leptin (previously reported data) and to CRP, varied markedly when expressed as a function of adiposity. Multiple regression models confirmed the strong relationship of adiponectin to insulin sensitivity, as well as the relationships of CRP to adiposity and insulin sensitivity. Glyburide treatment of diabetes decreased CRP and did so even though body weight increased. We conclude that both CRP and adiponectin correlate strongly to SI. CRP, in contrast to adiponectin, is far more dependent on adiposity. The relationship between CRP (like leptin) and gender depends on how CRP is expressed relative to adiposity. Our data raise the possibility that gender differences in adiponectin may be lost in diabetes. Finally, pharmacol. treatment of diabetes may modulate CRP independent of adiposity.

IT **657-24-9**, Metformin
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(adiponectin and C-reactive **protein** in obesity, type 2 **diabetes**, and monodrug therapy)

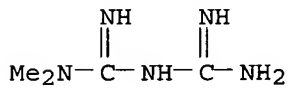
RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 40 THERE ARE 40 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 5 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:828364 HCAPLUS
DOCUMENT NUMBER: 141:374602
TITLE: Activation of the AMP-activated Protein Kinase by the Anti-diabetic Drug Metformin in Vivo: Role of mitochondrial reactive nitrogen species
AUTHOR(S): Zou, Ming-Hui; Kirkpatrick, Stacy S.; Davis, Bradley

J.; Nelson, John S.; Wiles, Walter G., IV; Schlattner, Uwe; Neumann, Dietbert; Brownlee, Michael; Freeman, Michael B.; Goldman, Mitch H.
CORPORATE SOURCE: Vascular Research Laboratory, Graduate School of Medicine, University of Tennessee, Knoxville, TN, 37920, USA
SOURCE: J. Biol. Chem. (2004), 279(42), 43940-43951
CODEN: JBCHA3; ISSN: 0021-9258
PUBLISHER: American Society for Biochemistry and Molecular Biology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Metformin, one of the most commonly used drugs for the treatment of type II diabetes, was recently found to exert its therapeutic effects, at least in part, by activating the AMP-activated protein kinase (AMPK). However, the site of its action, as well as the mechanism to activate AMPK, remains elusive. Here the authors report how metformin activates AMPK. In cultured bovine aortic endothelial cells, metformin dose-dependently activated AMPK in parallel with increased detection of reactive nitrogen species (RNS). Further, either depletion of mitochondria or adenoviral overexpression of superoxide dismutases, as well as inhibition of nitric-oxide synthase, abolished the metformin-enhanced phosphorylations and activities of AMPK, implicating that activation of AMPK by metformin might be mediated by the mitochondria-derived RNS. Furthermore, administration of metformin, which increased 3-nitrotyrosine staining in hearts of C57BL6, resulted in parallel activation of AMPK in the aorta and hearts of C57BL6 mice but not in those of endothelial nitric-oxide synthase (eNOS) knockout mice in which metformin had no effect on 3-nitrotyrosine staining. Because the eNOS knockout mice expressed normal levels of AMPK-α that was activated by 5-aminoimidazole-4-carboxamide riboside, an AMPK agonist, these data indicate that RNS generated by metformin is required for AMPK activation in vivo. In addition, metformin significantly increased the co-immunopptn. of AMPK and its upstream kinase, LKB1, in C57BL6 mice administered to metformin in vivo. Using pharmacol. and genetic inhibitors, the authors found that inhibition of either c-Src or PI3K abolished AMPK that was enhanced by metformin. The authors conclude that activation of AMPK by metformin might be mediated by mitochondria-derived RNS, and activation of the c-Src/PI3K pathway might generate a metabolite or other mol. inside the cell to promote AMPK activation by the LKB1 complex.
IT **657-24-9**, Metformin
RL: DMA (Drug mechanism of action); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(activation of AMP-activated **protein** kinase by the anti-**diabetic** drug metformin in vivo and role of mitochondrial reactive nitrogen species)
RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 51 THERE ARE 51 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 6 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2004:203796 HCAPLUS

DOCUMENT NUMBER: 140:253571
TITLE: Preparation of N-phenyl or N-heterocyclyldibenzylamine compounds as inhibitors of cholesteryl ester transfer protein (CETP) and medicinal use thereof
INVENTOR(S): Maeda, Kimiya; Nagamori, Hironobu; Nakamura, Hiroshi; Shinkai, Hisashi; Suzuki, Yasunori; Takahashi, Daisuke; Taniguchi, Toshio
PATENT ASSIGNEE(S): Japan Tobacco Inc., Japan
SOURCE: PCT Int. Appl., 207 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.		DATE
WO 2004020393	A1	20040311	WO 2003-JP11041		20030829
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CA 2464846	AA	20040311	CA 2003-2464846		20030829
BR 2003006208	A	20041013	BR 2003-6208		20030829
JP 2004323504	A2	20041118	JP 2003-308156		20030829
JP 3630676	B2	20050316			
EP 1533292	A1	20050525	EP 2003-791414		20030829
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK					
TR 200401413	T1	20050621	TR 2004-200401413		20030829
ZA 2004003137	A	20050425	ZA 2004-3137		20040423
US 2005059810	A1	20050317	US 2004-503185		20041012
PRIORITY APPLN. INFO.:			JP 2002-255604	A	20020830
			JP 2003-107161	A	20030410
			WO 2003-JP11041	W	20030829

OTHER SOURCE(S): MARPAT 140:253571
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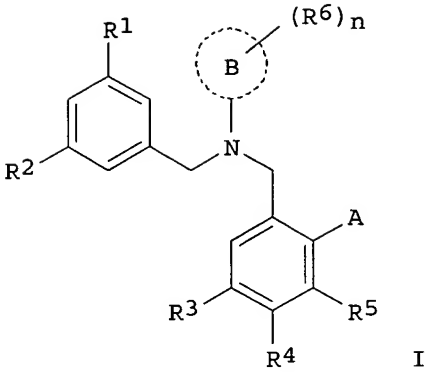


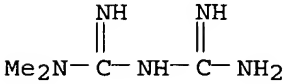
I

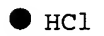
AB Dibenzylamine compds. represented by the general formula (I) [R1, R2 = halo, NO2, cyano, C1-6 alkyl, halo-C1-6 alkyl; R3, R4, R5 = H, halo, each optionally halo-substituted C1-6 alkyl, C1-6 alkylthio, or C1-6 alkoxy; or R3 and R4 or R4 and R5 together with the carbon atoms bonded thereto form an (un)substituted halo- or heterocyclic ring; A = NR7R8; wherein R7, R8 = H, each (un)substituted C1-6 alkyl or C4-10 cycloalkyl, etc.; the ring B = aryl or heterocyclyl; R6 = H, halo, NO2, NH2, HO, cyano, acyl, C1-6 alkoxy, (un)substituted C2-6 alkenyl; n = an integer of 1-3] or prodrugs thereof or pharmaceutically acceptable salts thereof are prepared These compds. have selective and potent CETP inhibitory activity, which results in lowering intermediate-d. lipoprotein (IDL), very low d. lipoprotein (VLDL), and low d. lipoprotein (LDL) which promote arteriosclerosis, and increasing high d. lipoprotein (HDL), and are hence usable as, e.g., therapeutic or preventive drugs for hyperlipemia and arteriosclerosis. Thus, 17 mg NaH was added to a solution of 132 mg N-[3-(N-cyclopentylmethyl-N-ethylamino)-5,6,7,8-tetrahydronaphthalen-2-ylmethyl]-(2-methyl-2H-tetrazol-5-yl)amine in 2 mL DMF, followed by adding 114 mg 3-bromomethyl-5-trifluoromethylbenzonitrile, and the resulting mixture was stirred at room temperature overnight to give, after workup and silica gel chromatog., 44% 3-[[N-[3-(N-cyclopentylmethyl-N-ethylamino)-5,6,7,8-tetrahydronaphthalen-2-ylmethyl]-N-(2-methyl-2H-tetrazol-5-yl)amino]methyl]-5-trifluoromethylbenzonitrile (II). II in vitro inhibited the activity of CETP in whole blood plasma with IC50 of 0.08 μM.

IT **1115-70-4**, Metformin hydrochloride **1190-53-0**, Buformin hydrochloride
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**antidiabetic**, combination therapy; preparation of N-Ph or N-heterocyclyldibenzylamine compds. as inhibitors of cholesteryl ester transfer **protein** (CETP) for treatment or prevention of hyperlipemia and arteriosclerosis)

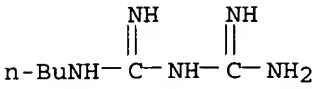
RN 1115-70-4 HCAPLUS

CN Imidodicarbonimidic diamide, N,N-dimethyl-, monohydrochloride (9CI) (CA INDEX NAME)





RN 1190-53-0 HCAPLUS
CN Imidodicarbonimidic diamide, N-butyl-, monohydrochloride (9CI) (CA INDEX NAME)



● HCl

REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

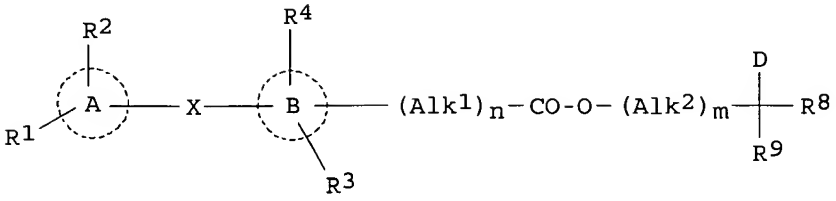
L8 ANSWER 7 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:696857 HCAPLUS
DOCUMENT NUMBER: 139:230479
TITLE: Preparation of [4-(1,1'-biphenyl-2-ylcarbonylamino or benzoylamino)phenyl]acetic acid esters as microsomal triglyceride transfer protein (MTP) inhibitors
INVENTOR(S): Hagiwara, Atsushi; Oe, Yasuhiro; Odani, Naoya; Watanabe, Shizue; Ikenogami, Taku; Kawai, Takashi; Madono, Kenya; Taniguchi, Toshio
PATENT ASSIGNEE(S): Japan Tobacco Inc., Japan
SOURCE: PCT Int. Appl., 561 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003072532	A1	20030904	WO 2003-JP2398	20030228
W: AE, AG, AL, AM, AU, AZ, BA, BB, BR, BY, BZ, CA, CN, CO, CR, CU, DM, DZ, EC, GD, GE, HR, ID, IL, IN, IS, KG, KR, KZ, LC, LK, LR, LT, LV, MA, MD, MG, MK, MN, MX, NO, NZ, OM, PH, PL, RO, RU, SC, SG, TJ, TM, TN, TT, UA, US, UZ, VC, VN, YU, ZA				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2460682	AA	20030904	CA 2003-2460682	20030228
JP 2003321424	A2	20031111	JP 2003-53869	20030228
JP 3662566	B2	20050622		
BR 2003006292	A	20040824	BR 2003-6292	20030228
EP 1479666	A1	20041124	EP 2003-743078	20030228
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, HU, SK				
ZA 2004002275	A	20050423	ZA 2004-2275	20040323
NO 2004001872	A	20040506	NO 2004-1872	20040506
US 2005075367	A1	20050407	US 2004-492831	20041008
JP 2005194281	A2	20050721	JP 2005-19579	20050127
JP 2005220132	A2	20050818	JP 2005-19739	20050127
JP 2005220133	A2	20050818	JP 2005-20179	20050127
PRIORITY APPLN. INFO.:			JP 2002-53876 A	20020228

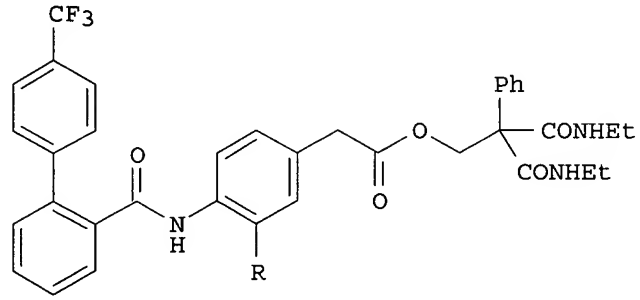
JP 2003-53869 A3 20030228
WO 2003-JP2398 W 20030228

OTHER SOURCE(S): MARPAT 139:230479

GI



I



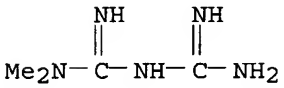
II

AB The title compds. [I; R1, R2 = H, C1-6 alkyl, C3-7 cycloalkyl, C1-6 alkoxy, halo-C1-6 alkyl, halo-C1-6 alkoxy, each (un)substituted C6-14 aryl, C7-16 aralkyl, C6-14 aryloxy, C7-16 aryloxy, C7-16 aralkyloxy, C7-15 arylcarbonyl, heterocyclyl, or NH2 C2-7 alkoxycarbonyl, halo, C2-6 alkenyl; the ring A = C6-14 aryl, heterocyclyl, 9-oxofluorenyl, fluorenyl; X = CO2(CH2)n, each N-(un)substituted CONH(CH2)n or NHCO(CH2)n (wherein n = an integer of 0-3); R3, R4 = H, HO, halo, each (un)substituted C1-6 alkyl, heterocyclyl, or CONH2, C1-6 alkoxy, halo-C1-6 alkyl, C7-16 aralkyloxy, C1-6 acyl; the ring B = phenylene, C5-7 (aza)cycloalkanediyl, indolediyl, benzimidazolediyl, pyridinediyl, pyrimidinediyl, benzocycloalkanedilyl, quinolinediyl, etc.; Alkl1, Alkl2 = alkanediyl, alkenediyl; n, m = 0-3; D = C1-6 alkyl, C2-6 alkenyl, C2-7 alkoxycarbonyl, NR42COR43 (wherein R42 = H, C1-6 alkyl; R43 = C4-14 aryl, C7-16 aralkyl), etc.; R8, R9 = H, C1-6 alkyl, (un)substituted C6-14 aryl, CONH2, or NH2, succinimid-2-yl, hydroxy-C1-6 alkyl, CO2H or its ester, (CH2)sO2CR20 (wherein R20 = H, C1-6 alkyl, C3-7 cycloalkyl; s = 0-3)] or prodrugs thereof or pharmaceutically acceptable salts of either are prepared These compds. I electively inhibit microsomal triglyceride transfer protein (MTP) of small intestine, are metabolized in blood or liver, and residual amount of MTP inhibitors is small enough not to substantially inhibit liver MTP and hence causes no side effects such as a fatty liver. They are useful for prevention or treatment of hyperlipidemia, arteriosclerosis, coronary artery diseases, obesity, diabetes, or hypertension. Thus, 519 mg 4-[(4'-trifluoromethyl-1,1'-biphenyl-2-ylcarbonyl)amino]phenylacetic acid (preparation given), 317 mg 2-hydroxymethyl-2-phenylmalonic acid diethylamide pg, and 268 mg 1-ethyl-3-(3-dimethylaminopropyl)carbodiimide hydrochloride were dissolved in 5 mL CH2Cl2 and stirred at room temperature for 6 h to give, after distillation of the solvent and silica gel chromatog., 725 mg 4-[(4'-trifluoromethyl-1,1'-biphenyl-2-ylcarbonyl)amino]phenylacetic acid 2,2-bis(ethylcarbamoyl)-2-phenylethyl ester (II; R = H). II (R = H) and II (R = Me) inhibited the triglyceride transport between liposomes by MTP with IC50 of 0.6 and 0.39 nM, resp., and the secretion of apolipoprotein B

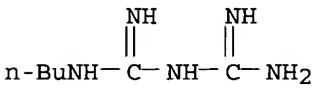
from HepG2 cell with IC50 of 0.65 and 0.46, resp. Pharmaceutical formulations, e.g. a tablet containing 2-[[2-[4-[(4'-trifluoromethyl-1,1'-biphenyl-2-ylcarbonyl)amino]-3-(pyrrolidinocarbonyl)phenyl]acetoxy]methyl]-2-phenylmalonic acid di-Et ester, were described.

IT **1115-70-4**, Metformin hydrochloride **1190-53-0**, Buformin hydrochloride
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**antidiabetic** agent, coadministration drugs containing; preparation of [(biphenylylcarbonylamino or benzoylamino)phenyl]acetic acid esters as microsomal triglyceride transfer **protein** (MTP) inhibitors for treatment or prevention of diseases)

RN 1115-70-4 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl-, monohydrochloride (9CI) (CA INDEX NAME)



RN 1190-53-0 HCAPLUS
CN Imidodicarbonimidic diamide, N-butyl-, monohydrochloride (9CI) (CA INDEX NAME)



REFERENCE COUNT: 13 THERE ARE 13 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 8 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:591022 HCAPLUS
DOCUMENT NUMBER: 139:145009
TITLE: cDNA and protein sequences for the UCP modifier proteins involved in the regulation of energy homeostasis and organelle metabolism and their therapeutic and diagnostic uses
INVENTOR(S): Steuernagel, Arnd; Molitor, Andreas; Eulenberg, Karsten; Broenner, Guenter
PATENT ASSIGNEE(S): Develogen Aktiengesellschaft Fuer Entwicklungsbiologische Forschung, Germany
SOURCE: PCT Int. Appl., 144 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 3
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003061681	A2	20030731	WO 2003-EP738	20030124
WO 2003061681	A3	20040923		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW

RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.:			
	EP 2002-1806	A	20020125
	EP 2002-3473	A	20020214
	EP 2002-4687	A	20020228
	EP 2002-9475	A	20020425
	EP 2002-13329	A	20020618
	EP 2002-29081	A	20021230

AB This invention relates to identifying mammalian **proteins** and enzymes playing a role in energy homeostasis and the organelle metabolism and characterizing cDNAs encoding them. The genes were first identified in Drosophila melanogaster as affecting body triglyceride content in the UCP (uncoupling **protein**) modifier screen. The UCP modifier genes were cloned and mammalian homologs identified by BLAST querying of sequence databases. The **proteins** for the UCP modifier genes are: Optic atrophy 1 **protein**, cornichon-like, IGF-II **mRNA**-binding **protein** 3, neuralized-like, KIAA1094 **protein**, casein kinase (delta and epsilon), glutamate dehydrogenase, kraken homolog, sirtuin 1, escargot homolog, human KIAA1585 **protein**, CG11940 homolog, dappled homolog, CG11753 homolog, human KIAA0095 **protein**, **formin**-binding **protein** 21. The invention also relates to the use of these sequences in the diagnosis, study, prevention, and treatment of diseases and disorders related to body-weight regulation and thermogenesis, for example, but not limited to, metabolic diseases such as obesity as well as related disorders such as eating disorder, cachexia, **diabetes** mellitus, hypertension, coronary heart disease, hypercholesterolemia, dyslipidemia, osteoarthritis, gallstones, cancers of the reproductive organs, and sleep apnea.

IT **572928-99-5**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(amino acid sequence; cDNA and **protein** sequences for UCP modifier **proteins** involved in regulation of energy homeostasis and organelle metabolism and their therapeutic and diagnostic uses)

RN 572928-99-5 HCAPLUS

CN Protein (human CG4291/formin-binding protein 21-sequence-homolog) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

IT **572928-97-3**
RL: BSU (Biological study, unclassified); DGN (Diagnostic use); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**nucleotide** sequence; cDNA and **protein** sequences for UCP modifier **proteins** involved in regulation of energy homeostasis and organelle metabolism and their therapeutic and diagnostic

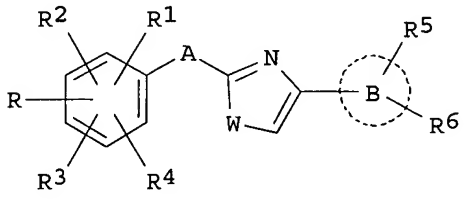
uses)
RN 572928-97-3 HCAPLUS
CN DNA (human protein CG4291/formin-binding protein 21-sequence-homolog cDNA) (9CI) (CA INDEX NAME)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

L8 ANSWER 9 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:454306 HCAPLUS
DOCUMENT NUMBER: 139:36522
TITLE: Preparation of azole compounds as protein tyrosine phosphatase 1B inhibitors
INVENTOR(S): Inaba, Takashi; Ikemoto, Tomoyuki; Sakata, Shohei; Maegawa, Hiroshi; Kashiwagi, Atsunori
PATENT ASSIGNEE(S): Japan Tobacco Inc., Japan
SOURCE: PCT Int. Appl., 200 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: Japanese
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003048140	A1	20030612	WO 2002-JP12673	20021203
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
CA 2469228	AA	20030612	CA 2002-2469228	20021203
JP 2003231679	A2	20030819	JP 2002-351730	20021203
EP 1452530	A1	20040901	EP 2002-783753	20021203
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR, BG, CZ, EE, SK				
US 2005065196	A1	20050324	US 2004-497492	20041029
PRIORITY APPLN. INFO.:			JP 2001-368567 A	20011203
			WO 2002-JP12673 W	20021203

OTHER SOURCE(S): MARPAT 139:36522
GI



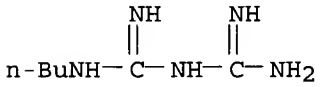
I

AB Azole compds. such as 2-amino-4-phenylthiazole derivs. represented by the general formula (I) [wherein W = S, O; R = CO2R7, -X1-A1-CO2R7, or tetrazolyl [wherein R = H, lower alkyl; X1 = O, NH, lower alkyl-imino, S,

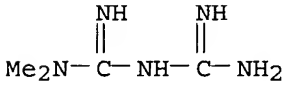
S(O), SO2]; R1, R2, R3, R4 = H, halo, HO, (un)substituted lower cycloalkylalkyloxy, (un)substituted aralkyloxy, cyano, NO2, lower (halo)alkoxy, lower (halo)alkoxy; A = -(CH2)m-X- [wherein X = (un)substituted NH, CH2, or CONH, CO]; the ring B = aryl or an aromatic heterocyclic group; R5 = H, halo, lower alkyl or alkoxy, cyano, NO2, lower haloalkyl, S(O)rR17 (wherein r = 0,1,2; R17 = lower alkyl, aryl); R6 = -(Y)s1-(A2)s-Z [wherein Y = O, S, SO, SO2, each (un)substituted NH, NHCO, NHSO2, SO2NH, or CH2, CO; A2 = lower alkylene optionally substituted by lower cycloalkyl; Z = lower cycloalkyl optionally substituted by (un)substituted Ph, each optionally substituted aryl, an aromatic heterocyclic group, or piperazinyl, indanyl]], prodrugs of the compds., or pharmaceutically acceptable salts of any of these are prepared The compds. I have protein tyrosine phosphatase 1B (PTP1B) inhibitory activity and are useful as therapeutic agents for diabetes, complications of diabetes, and hyperlipemia. Thus, reductive alkylation of 4-[N-[4-(4-aminophenyl)-2-thiazolyl]-N-methylaminomethyl]benzoic acid Me ester by 4-cyclohexylbenzaldehyde and sodium triacetoxyborohydride in AcOH and THF at room temperature for 3 h gave 4-[N-[4-[4-(4-cyclohexylbenzylamino)phenyl]-2-thiazolyl]-N-methylaminomethyl]benzoic acid Me ester which underwent N-methylation by di-Me sulfate and K2CO3 in N,N-dimethylacetamide at 50° for 1 h and at 60° for 1 h, saponification with a mixture of aqueous 1 N NaOH soln, THF, and MeOH, and acidification with aqueous 2 N HCl soln to give 4-[N-[4-[4-[N-(4-cyclohexylbenzyl)-N-methylamino]phenyl]-2-thiazolyl]-N-methylaminomethyl]benzoic acid (II). II inhibited PTP1B with IC50 of 0.32 μM and at 0.3 mg/kg p.o. lowered blood sugar in male ob/ob mice by 35% after 3 h. A tablet formulation containing II was described.

IT **692-13-7**, Buformin **1115-70-4**, Metformin hydrochloride
RL: THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**antidiabetic** containing; preparation of azole compds. as **protein** tyrosine phosphatase 1B inhibitors for treatment or prevention of **diabetes**, hyperlipidemia, or **diabetes** complications)

RN 692-13-7 HCAPLUS
CN Imidodicarbonimidic diamide, N-butyl- (9CI) (CA INDEX NAME)



RN 1115-70-4 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl-, monohydrochloride (9CI) (CA INDEX NAME)



REFERENCE COUNT: 14 THERE ARE 14 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

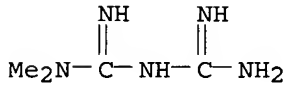
L8 ANSWER 10 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:395620 HCAPLUS

DOCUMENT NUMBER: 139:95209
TITLE: Effect of metformin and sulfonylurea on C-reactive protein level in well-controlled type 2 diabetics with metabolic syndrome
AUTHOR(S): Akbar, Daad Hassan
CORPORATE SOURCE: Department of Medicine, King Abdulaziz University Hospital, Jeddah, Saudi Arabia
SOURCE: Endocrine (2003), 20(3), 215-218
CODEN: EOCRE5; ISSN: 1355-008X
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The objective of this study was to examine the effect of the antihyperglycemic agents metformin (insulin sensitizer) and glibenclamide (insulin secretory agent) on the serum level of C-reactive protein (CRP) in well-controlled type 2 diabetics with metabolic syndrome. The participants were diabetic patients being followed in the medical outpatient clinic of King Abdulaziz University Hospital. The inclusion criteria were type 2 diabetics with the metabolic syndrome, well-controlled blood glucose on metformin alone or glibenclamide alone, and exclusion of major medical illness. Patients were divided into two groups according to the antihyperglycemic agent used. CRP level was measured 4-wk apart and the mean was calculated The following data were collected from the study groups: age, sex, body mass index (BMI), duration of diabetes, smoking history, presence of hypertension, hyperlipidemia, and mean CRP level. A total of 110 patients were studied, 65 using metformin and 45 using glibenclamide. CRP level was significantly lower in patients using metformin for blood glucose control compared with those using glibenclamide, 5.56 and 8.3 mg/L, resp. ($p = 0.01$). A significantly higher level was observed in hypertensive and hyperlipidemic patients compared with normotensive and normolipidemic, 5.3 vs. 3.2 mg/L and 7.1 vs. 4.3 mg/L, resp. ($p = 0.02$, 0.01). There was a statistically significant correlation between CRP and BMI ($r = 0.37$) and age ($r = 0.36$) (all $p = 0.01$). The data showed that metformin decreases the level of circulating CRP, a marker of inflammation, more than glibenclamide.

IT **657-24-9**, Metformin
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(effect of metformin and sulfonylurea (glibenclamide) on C-reactive **protein** level in well-controlled type 2 **diabetics** with metabolic syndrome)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

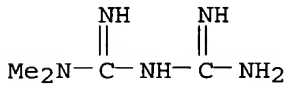
L8 ANSWER 11 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:596186 HCAPLUS
DOCUMENT NUMBER: 138:147497
TITLE: The antidiabetic drug metformin activates the AMP-activated protein kinase cascade via an adenine nucleotide-independent mechanism
AUTHOR(S): Hawley, Simon A.; Gadalla, Anne E.; Olsen, Grith

Skytte; Hardie, D. Grahame
CORPORATE SOURCE: Division of Molecular Physiology, School of Life Sciences and Wellcome Trust Biocentre, Dundee University, Dundee, DD1 5EH, UK
SOURCE: Diabetes (2002), 51(8), 2420-2425
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Metformin, a drug widely used to treat type 2 diabetes, was recently shown to activate the AMP-activated protein kinase (AMPK) in intact cells and in vivo. In this study we addressed the mechanism for this effect. In intact cells, metformin stimulated phosphorylation of the key regulatory site (Thr-172) on the catalytic (α) subunit of AMPK. It did not affect phosphorylation of this site by either of two upstream kinases in cell-free assays, although we were able to detect an increase in upstream kinase activity in exts. of metformin-treated cells. Metformin has been reported to be an inhibitor of complex 1 of the respiratory chain, but we present evidence that activation of AMPK in two different cell types is not a consequence of depletion of cellular energy charge via this mechanism. Whereas we have not established the definitive mechanism by which metformin activates AMPK, our results show that the mechanism is different from that of the existing AMPK-activating agent, 5-aminoimidazole-4-carboxamide (AICA) riboside. Metformin therefore represents a useful new tool to study the consequences of AMPK activation in intact cells and in vivo. Our results also show that AMPK can be activated by mechanisms other than changes in the cellular AMP-to-ATP ratio.

IT **657-24-9**, Metformin
RL: PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**antidiabetic** metformin activates AMP-activated **protein** kinase cascade via an adenine **nucleotide** -independent mechanism)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 32 THERE ARE 32 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

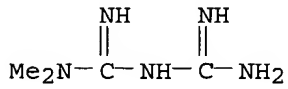
L8 ANSWER 12 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:521648 HCAPLUS
DOCUMENT NUMBER: 137:103709
TITLE: Metformin increases AMP-activated protein kinase activity in skeletal muscle of subjects with type 2 diabetes
AUTHOR(S): Musi, Nicolas; Hirshman, Michael F.; Nygren, Jonas; Svanfeldt, Monika; Bavenholm, Peter; Rooyackers, Olav; Zhou, Gaochao; Williamson, Joanne M.; Ljunqvist, Olle; Efendic, Suad; Moller, David E.; Thorell, Anders; Goodyear, Laurie J.
CORPORATE SOURCE: Research Division, Joslin Diabetes Center, Brigham and Women's Hospital and Harvard Medical School, Boston, MA, USA

SOURCE: Diabetes (2002), 51(7), 2074-2081
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Metformin is an effective hypoglycemic drug that lowers blood glucose concns. by decreasing hepatic glucose production and increasing glucose disposal in skeletal muscle; however, the mol. site of metformin action is not well understood. AMP-activated protein kinase (AMPK) activity increases in response to depletion of cellular energy stores, and this enzyme has been implicated in the stimulation of glucose uptake into skeletal muscle and the inhibition of liver gluconeogenesis. We recently reported that AMPK is activated by metformin in cultured rat hepatocytes, mediating the inhibitory effects of the drug on hepatic glucose production In the present study, we evaluated whether therapeutic doses of metformin increase AMPK activity in vivo in subjects with type 2 diabetes. Metformin treatment for 10 wk significantly increased AMPK α2 activity in the skeletal muscle, and this was associated with increased phosphorylation of AMPK on Thr172 and decreased acetyl-CoA carboxylase-2 activity. The increase in AMPK α2 activity was likely due to a change in muscle energy status because ATP and phosphocreatine concns. were lower after metformin treatment. Metformin-induced increases in AMPK activity were associated with higher rates of glucose disposal and muscle glycogen concns. These findings suggest that the metabolic effects of metformin in subjects with type 2 diabetes may be mediated by the activation of AMPK α2.

IT **657-24-9**, Metformin
RL: DMA (Drug mechanism of action); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(metformin increases AMP-activated **protein** kinase activity in skeletal muscle of subjects with type 2 **diabetes**)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 62 THERE ARE 62 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 13 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:102996 HCAPLUS
DOCUMENT NUMBER: 136:272998
TITLE: Troglitazone but not metformin restores insulin-stimulated phosphoinositide 3-kinase activity and increases p110β protein levels in skeletal muscle of type 2 diabetic subjects
AUTHOR(S): Kim, Young-Bum; Ciaraldi, Theodore P.; Kong, Alice; Kim, Dennis; Chu, Neelima; Mohideen, Pharis; Mudaliar, Sunder; Henry, Robert R.; Kahn, Barbara B.
CORPORATE SOURCE: Diabetes Unit, Division of Endocrinology and Metabolism, Department of Medicine, Beth Israel Deaconess Medical Center, Boston, MA, 02215, USA
SOURCE: Diabetes (2002), 51(2), 443-448
CODEN: DIAEAZ; ISSN: 0012-1797
PUBLISHER: American Diabetes Association
DOCUMENT TYPE: Journal

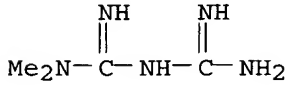
LANGUAGE: English

AB Insulin stimulation of phosphatidylinositol (PI) 3-kinase activity is defective in skeletal muscle of type 2 diabetic individuals. We studied the impact of antidiabetic therapy on this defect in type 2 diabetic subjects who failed glyburide treatment by the addition of troglitazone (600 mg/day) or metformin (2,550 mg/day) therapy for 3-4 mo. Improvement in glycemic control was similar for the two groups, as indicated by changes in fasting glucose and HbA1c levels. Insulin action on whole-body glucose disposal rate (GDR) was determined before and after treatment using the hyperinsulinemic (300 mU · m-2 · min-1) euglycemic (5.0-5.5 mmol/l) clamp technique. Needle biopsies of vastus lateralis muscle were obtained before and after each 3-h insulin infusion. Troglitazone treatment resulted in a 35±9% improvement in GDR ($P < 0.01$), which was greater than ($P < 0.05$) the 22±13% increase ($P < 0.05$) after metformin treatment. Neither treatment had any effect on basal insulin receptor substrate-1 (IRS-1)-associated PI 3-kinase activity in muscle. However, insulin stimulation of PI 3-kinase activity was augmented nearly threefold after troglitazone treatment (from 67±22% stimulation over basal pre-treatment to 211±62% post-treatment, $P < 0.05$), whereas metformin had no effect. The troglitazone effect on PI 3-kinase activity was associated with a 46±22% increase ($P < 0.05$) in the amount of the p110β catalytic subunit of PI 3-kinase. Insulin-stimulated Akt activity also increased after troglitazone treatment (from 32±8 to 107±32% stimulation, $P < 0.05$) but was unchanged after metformin therapy. Protein expression of other key insulin signaling mols. (IRS-1, the p85 subunit of PI 3-kinase, and Akt) was unaltered after either treatment. We conclude that the mechanism for the insulin-sensitizing effect of troglitazone, but not metformin, involves enhanced PI 3-kinase pathway activation in skeletal muscle of obese type 2 diabetic subjects.

IT **657-24-9**, Metformin
RL: DMA (Drug mechanism of action); PAC (Pharmacological activity); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(troglitazone but not metformin restores insulin-stimulated phosphoinositide 3-kinase activity and increases p110β **protein** levels in skeletal muscle of type 2 **diabetic** subjects)

RN 657-24-9 HCAPLUS

CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 53 THERE ARE 53 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 14 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 2001:764220 HCAPLUS

DOCUMENT NUMBER: 136:79553

TITLE: Role of AMP-activated protein kinase in mechanism of metformin action

AUTHOR(S): Zhou, Gaochao; Myers, Robert; Li, Ying; Chen, Yuli; Shen, Xiaolan; Fenyk-Melody, Judy; Wu, Margaret; Ventre, John; Doebber, Thomas; Fujii, Nobuharu; Musi, Nicolas; Hirshman, Michael F.; Goodyear, Laurie J.; Moller, David E.

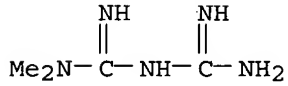
CORPORATE SOURCE: Departments of Molecular Endocrinology, Metabolic Disorders, Merck Research Laboratories, Rahway, NJ,

07065, USA
SOURCE: Journal of Clinical Investigation (2001), 108(8), 1167-1174
CODEN: JCINAO; ISSN: 0021-9738
PUBLISHER: American Society for Clinical Investigation
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Metformin is a widely used drug for treatment of type 2 diabetes with no defined cellular mechanism of action. Its glucose-lowering effect results from decreased hepatic glucose production and increased glucose utilization. Metformin's beneficial effects on circulating lipids have been linked to reduced fatty liver. AMP-activated protein kinase (AMPK) is a major cellular regulator of lipid and glucose metabolism Here we report that metformin activates AMPK in hepatocytes; as a result, acetyl-CoA carboxylase (ACC) activity is reduced, fatty acid oxidation is induced, and expression of lipogenic enzymes is suppressed. Activation of AMPK by metformin or an adenosine analog suppresses expression of SREBP-1, a key lipogenic transcription factor. In metformin-treated rats, hepatic expression of SREBP-1 (and other lipogenic) mRNAs and protein is reduced; activity of the AMPK target, ACC, is also reduced. Using a novel AMPK inhibitor, we find that AMPK activation is required for metformin's inhibitory effect on glucose production by hepatocytes. In isolated rat skeletal muscles, metformin stimulates glucose uptake coincident with AMPK activation. Activation of AMPK provides a unified explanation for the pleiotropic beneficial effects of this drug; these results also suggest that alternative means of modulating AMPK should be useful for the treatment of metabolic disorders.

IT **657-24-9**, Metformin
RL: DMA (Drug mechanism of action); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(role of AMP-activated **protein** kinase in mechanism of metformin **antidiabetic** action)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



REFERENCE COUNT: 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

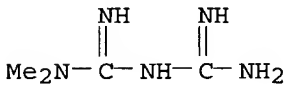
L8 ANSWER 15 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2000:788558 HCAPLUS
DOCUMENT NUMBER: 134:360944
TITLE: Effects of oral hypoglycemic agents and diet on protein metabolism in type 2 diabetes
AUTHOR(S): Gougeon, Rejeanne; Styhler, Karin; Morais, Jose A.; Jones, Peter J. H.; Marliss, Errol B.
CORPORATE SOURCE: McGill Nutrition and Food Science Center, McGill University, Montreal, QC, H3A 1A1, Can.
SOURCE: Diabetes Care (2000), 23(1), 1-8
CODEN: DICAD2; ISSN: 0149-5992
PUBLISHER: American Diabetes Association, Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB We tested whether oral hypoglycemic agents (OHA), gliclazide with or without metformin, during an isoenergetic (ISO) and then a low-energy diet

(LED) improve the altered kinetics of whole-body protein metabolism in type 2 diabetes. A total of 13 type 2 diabetic patients (aged 51±2 yr, weight 110±5 kg, BMI 41±1 kg/m2, fasting glucose [FSG] 11.5±0.9 mmol/l) (means ± SEM) and 10 obese control subjects (48±3 yr, 98±6 kg, 37±2 kg/m2, FSG 5.5±0.3 mmol/l) consumed an ISO, 1.5 g · kg-1 · day-1 protein for a body weight corresponding to a BMI of 25 (BMI25), a formula diet (7 days for obese control subjects, 15 days for diabetic patients), and then a 28-day LED with 50% of the energy of ISO but the same protein intake (101±2 g/day). OHAs were given during ISO (days 8-15) and LED. On days 6-8 (and 12-14 for diabetic subjects) of ISO and 26-28 of LED, the 60-h oral 15N-glycine method was used to obtain nitrogen flux (Q), synthesis (S), and breakdown (B). Muscle protein catabolism was estimated from Nτ-methylhistidine (3MH) excretion. During ISO with hyperglycemia, Q, and B adjusted for fat-free mass, sex, and age were higher and nitrogen balance and net endogenous protein synthesis (S-B) lower than in control subjects ($P < 0.05$). OHA decreased FSG (9±1 mmol/l) and 3MH and increased plasma insulin-to-glucose ratio, nitrogen retention, and S-B to levels in control subjects. The change in S-B correlated with that in FSG ($r = -0.845$, $P = 0.001$) and in fasting plasma C-peptide ($r = 0.852$, $P = 0.0005$). With LED and OHA, weight decreased 6.3 kg, glycemia reached near-normal levels, and nitrogen equilibrium was maintained; Q decreased by 7%, S and B by 11% ($P < 0.05$) to values found in control subjects. OHA during ISO corrected protein turnover in relation to glycemia and plasma C-peptide. The LED maintained protein homeostasis in obese control subjects and, in diabetes patients with OHA, normalized protein metabolism These findings have implications for diet and OHA prescription.

IT **657-24-9**, Metformin
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(effects of oral **hypoglycemic** agents and diet on **protein** metabolism in type 2 **diabetes**)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



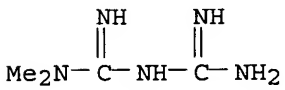
REFERENCE COUNT: 39 THERE ARE 39 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L8 ANSWER 16 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1993:641175 HCAPLUS
DOCUMENT NUMBER: 119:241175
TITLE: Metformin increases glucose transporter protein and gene expression in human fibroblasts
AUTHOR(S): Hamann, Andreas; Benecke, Heike; Greten, Heiner; Matthaei, Stephan
CORPORATE SOURCE: Dep. Med., Univ.-Krankenhaus Eppendorf, Hamburg, 20246, Germany
SOURCE: Biochemical and Biophysical Research Communications (1993), 196(1), 382-7
CODEN: BBRCA9; ISSN: 0006-291X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB To study the effect of the antihyperglycemic drug metformin on glucose

transporter protein and gene expression, skin fibroblasts obtained from normal and diabetic volunteers were grown in culture and incubated with metformin at various concentration for up to 16 days. Metformin caused a dose and time dependent increase in the glucose transporter GLUT1 number with a maximum at a concentration of 10 μg metformin given over 4 days. This was accompanied by an increase in GLUT1 mRNA, suggesting that metformin has a stimulating effect on glucose transporter gene expression. No difference was observed between cells obtained from type II diabetic patients and those from controls. Apparently, in human fibroblasts, GLUT1 de novo synthesis is involved in the long term effect of metformin on glucose transport.

IT **657-24-9**, Metformin
RL: BIOL (Biological study)
(glucose transporter **protein** GLUT 1 and gene expression increase by, **diabetes** effect on, in human cells)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)

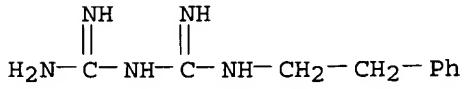


L8 ANSWER 17 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1983:416373 HCAPLUS
DOCUMENT NUMBER: 99:16373
TITLE: Antidiabetic behavior of biguanides
AUTHOR(S): Vicente-Pedros, F.; Trejueque Monge, J.; Tomas Vert, F.
CORPORATE SOURCE: Fac. Chem., Univ. Valencia, Burjasot, Spain
SOURCE: Journal of Pharmaceutical Sciences (1983), 72(5), 565-7
CODEN: JPMSAE; ISSN: 0022-3549
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The existence of active electron pairs on some N atoms in phenformin (I) [**114-86-3**] is inferred from the presence of a H catalytic polarog. wave. This finding emphasizes the ability of biguanides to form H bridges with other mol. species such as amino acids and **proteins**, as well as to form coordination complexes with Zn and other metallic cations by means of these electron pairs. The **antidiabetic** action of I and other related biguanides can be explained in terms of competition between these mols. and insulin [9004-10-8] to coordinate cationic oligoelements, thereby freeing insulin mols., together with their ability to form H bonds between the biguanide moiety and insulin itself.

IT **114-86-3**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(**antidiabetic** activity of, mechanism of)

RN 114-86-3 HCAPLUS
CN Imidodicarbonimidic diamide, N-(2-phenylethyl)- (9CI) (CA INDEX NAME)



L8 ANSWER 18 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1982:538431 HCAPLUS
DOCUMENT NUMBER: 97:138431
TITLE: Effect of metformin on insulin binding to receptors in cultured human lymphocytes and cancer cells
AUTHOR(S): Pezzino, V.; Trischitta, V.; Purrello, F.; Vigneri, R.
CORPORATE SOURCE: Ist. Patol. Med., Univ. Catania, Catania, I-95124, Italy
SOURCE: Diabetologia (1982), 23(2), 131-5
CODEN: DBTGAJ; ISSN: 0012-186X
DOCUMENT TYPE: Journal
LANGUAGE: English
AB metformin **[657-24-9]** Increased insulin [9004-10-8] binding in vitro to IM-9 lymphocytes and MCF-7 human breast cancer cells. The latter cell line was more sensitive to metformin, with a significant effect apparent at a metformin concentration of 7.7 + 10-6 mol/L, similar to the levels reached in patients treated with this drug. When compared with phenformin **[114-86-3]**, metformin was less active in increasing insulin binding to cultured cells, the ratio between the 2 drug responses being similar to that of their therapeutic dosage in patients. Insulin binding increment due to metformin was reversible, was not dependent on new **protein** synthesis and was evident also in IM-9 lymphocytes that had been down-regulated by pre-incubation with insulin (10-7 mol/L). This effect of metformin on insulin binding to receptors may contribute to the **hypoglycemic** effect of this agent in patients.

L8 ANSWER 19 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1982:466243 HCAPLUS
DOCUMENT NUMBER: 97:66243
TITLE: Metformin increases the number of insulin receptors in human erythrocytes
AUTHOR(S): Holle, A.; Dreyer, M.; Kuehnau, J.; Mangels, W.; Maack, P.; Siemers, U.; Ruediger, H. W.
CORPORATE SOURCE: I. Med. Klin., Univ. Hamburg, Hamburg, Fed. Rep. Ger.
SOURCE: Proceedings of the Serono Symposia (1981), 41(Curr. Views Insulin Recept.), 601-5
CODEN: PSSYDG; ISSN: 0308-5503
DOCUMENT TYPE: Journal
LANGUAGE: English
AB On incubation of erythrocytes from healthy human subjects with metformin **[657-24-9]**, no change was observed in the high affinity-low capacity insulin [9004-10-8] receptor sites; however, the number of low affinity-high capacity sites increased and insulin binding at high insulin concns. was increased. Similar results were observed in subjects given metformin orally. The **antidiabetic** probably increased the low affinity-high capacity insulin receptors due to unmasking, since no de novo **protein** synthesis occurs in erythrocytes.

L8 ANSWER 20 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1980:437529 HCAPLUS
DOCUMENT NUMBER: 93:37529
TITLE: Effects of metformin on the changes in blood insulin and glucagon induced by a protein meal in normal and diabetic subjects
AUTHOR(S): Ferlito, S.; Fichera, C.
CORPORATE SOURCE: Ist. Patol., Univ. Catania, Catania, Italy
SOURCE: Progresso Medico (Rome) (1979), 35(18), 786-93
CODEN: PRMOAE; ISSN: 0370-1514
DOCUMENT TYPE: Journal

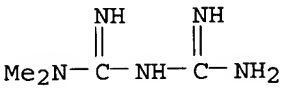
LANGUAGE: Italian

AB Plasma insulin [9004-10-8] and glucagon [9007-92-5] concns. increased in response to a **protein** meal in both normal subjects and partially compensated adult **diabetics**. The rise in insulin was inhibited by metformin [**657-24-9**] (1 g, orally) in the normal persons but not in the **diabetics**, whereas the rise in glucagon was inhibited by metformin in both groups. The low **hypoglycemic** action of metformin in **diabetics** might be due to its lack of effect on insulin, with consequent increase in the plasma insulin-to-glucagon ratio.

IT **657-24-9**
RL: BIOL (Biological study)
(glucagon and insulin of blood plasma response to **protein** meal inhibition by, in **diabetes**)

RN 657-24-9 HCAPLUS

CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



L8 ANSWER 21 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1980:69701 HCAPLUS
DOCUMENT NUMBER: 92:69701
TITLE: The influence of Meguan on vitamin B12 absorption
AUTHOR(S): Deutsch, G.; Bacanu, G.; Drugarin, D.; Berger, E.
CORPORATE SOURCE: Diabets Clin., Inst. Med., Timisoara, Rom.
SOURCE: Timisoara Medicala (1979), 24(2), 51-2
CODEN: TIMEBY; ISSN: 0493-3079
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The intestinal absorption of vitamin B12 [68-19-9], as measured by the Schilling test, was below normal in 33% of **diabetics** taking the **antidiabetic** drug meguan [**1115-70-4**], whereas other **diabetics** not taking this drug had normal values in this test. Incubation of meguan with isolated rat pancreas increased tissue O consumption, decreased tissue accumulation of selenomethionine-75Se, and increased the **protein**-bound selenomethionine fraction. These effects may be related to the action of meguan in decreasing vitamin B12 absorption.

L8 ANSWER 22 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN

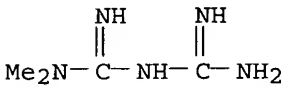
ACCESSION NUMBER: 1978:400617 HCAPLUS
DOCUMENT NUMBER: 89:617
TITLE: Effect of metformin on amino acids absorption in man
AUTHOR(S): Hafiez, A. A.; Ismail, A. A.; El-Kirdassy, Z. H.; Khater, R. A.
CORPORATE SOURCE: Fac. Med., Cairo Univ., Cairo, Egypt
SOURCE: Ain Shams Medical Journal (1977), 28(3-4), 183-8
CODEN: AIMJA9; ISSN: 0002-2144
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The effects of metformin [**657-24-9**] was studied on amino acid and **protein** absorption after ingestion of a **protein** meal (250 g skimmed cheese) in normal and **diabetic** volunteers. The rate of amino acid absorption was decreased and the time of peak blood amino acid N levels was extended by metformin in normal volunteers. In **diabetics**, amino acid absorption was enhanced. The fasting blood

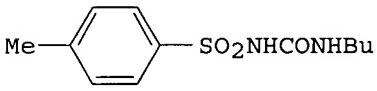
amino acid N level was decreased and increased by metformin in normal and **diabetic** volunteers, resp. The results are discussed with respect to the various processes involved in digestion.

IT **657-24-9**
RL: BIOL (Biological study)
(amino acid and **protein** absorption response to)

RN 657-24-9 HCAPLUS
CN Imidodicarbonimidic diamide, N,N-dimethyl- (9CI) (CA INDEX NAME)



L8 ANSWER 23 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1976:413723 HCAPLUS
DOCUMENT NUMBER: 85:13723
TITLE: The effect of oral antidiabetics on protein biosynthesis in vitro
AUTHOR(S): Tragl, K. H.; Machanek, Margarethe
CORPORATE SOURCE: I. Med. Universitaetsklin., Vienna, Austria
SOURCE: Arzneimittel-Forschung (1976), 26(3), 374-7
CODEN: ARZNAD; ISSN: 0004-4172
DOCUMENT TYPE: Journal
LANGUAGE: German
GI

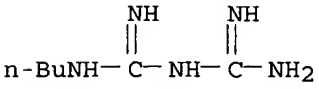


I

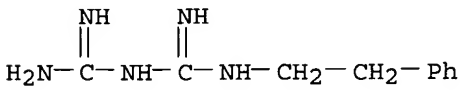
AB Tolbutamide (I) [64-77-7] (2 + 20 or 2 + 80 mg/kg/day) administered i.p. to normal or alloxan-**diabetic** rats inhibited **protein** synthesis by their isolated liver ribosomes through a direct effect on the ribosomes. Butylbiguanide [**692-13-7**] (2 + 12 or 2 + 36 mg/kg/day s.c.) inhibited **protein** synthesis by liver ribosomes of normal rats, but dose-dependently stimulated that of **diabetic** rats. The specific pattern of ribosome distribution in sucrose d. gradients was unaffected by I in normal and **diabetic** rats. However, butylbiguanide caused a decrease in the proportion of polysomes in livers of normal rats, but did not affect the proportion of polysomes in livers of **diabetic** rats (which was lower than in normal rats).

IT **692-13-7**
RL: BIOL (Biological study)
(**protein** formation by liver ribosomes response to)

RN 692-13-7 HCAPLUS
CN Imidodicarbonimidic diamide, N-butyl- (9CI) (CA INDEX NAME)



L8 ANSWER 24 OF 24 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1967:64016 HCAPLUS
DOCUMENT NUMBER: 66:64016
TITLE: Effects of three oral hypoglycemic agents on the incorporation of leucine-14C into protein by liver microsomes of normal and alloxan-diabetic rats
AUTHOR(S): McDonald, Hugh J.; DeChatelet, Lawrence R.
CORPORATE SOURCE: Stritch Sch. of Med., Loyola Univ., Chicago, IL, USA
SOURCE: Life Sciences (1967), 6(2), 183-9
CODEN: LIFSAK; ISSN: 0024-3205
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Tolbutamide, chlorpropamide, and phenethylbiguanide at concns. ≤10 micromoles/ml. depressed the incorporation of leucine-14C into protein when they were added in vitro to liver microsomes from both normal and alloxan-diabetic rats. The inhibition by the 3 hypoglycemic agents was quant. similar with respect to concentration, and the incorporation was much lower at all points with the microsomes from the diabetic rats than with the normal rat microsomes. In control expts. NaCl did not depress the incorporation of leucine-14C in rat liver microsomal prepns. These oral hypoglycemic agents alone probably do not alleviate the protein imbalance associated with diabetes mellitus.
IT **114-86-3**
RL: BIOL (Biological study)
(in **protein** formation by liver microsomes, in **diabetes**)
RN 114-86-3 HCAPLUS
CN Imidodicarbonimidic diamide, N-(2-phenylethyl)- (9CI) (CA INDEX NAME)



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L2 29 SEA FILE=HCAPLUS ABB=ON PLU=ON L1 OR FHOS
L3 259 SEA FILE=REGISTRY ABB=ON PLU=ON FORMIN/BI
L4 44779 SEA FILE=HCAPLUS ABB=ON PLU=ON L3 OR FORMIN
L5 1163 SEA FILE=HCAPLUS ABB=ON PLU=ON L4(L)(?DIABET? OR INSULIN(2A)RESIS? OR ?GLYCEM?)
L6 796 SEA FILE=HCAPLUS ABB=ON PLU=ON L4(L)(MRNA OR DNA OR ?NUCLE? OR PROTEIN)
L7 25 SEA FILE=HCAPLUS ABB=ON PLU=ON L6 AND L5
L8 24 SEA FILE=HCAPLUS ABB=ON PLU=ON L7 NOT L2
L10 11 SEA FILE=HCAPLUS ABB=ON PLU=ON L4(L)SPLEEN
L11 6 SEA FILE=HCAPLUS ABB=ON PLU=ON L10 NOT (L2 OR L8)

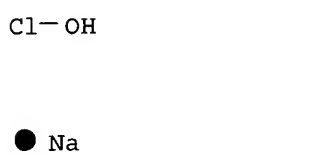
=> d ibib abs hitstr l11 1-6

L11 ANSWER 1 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2003:850466 HCAPLUS
DOCUMENT NUMBER: 140:3492
TITLE: Human leukocyte formin: a novel protein expressed in lymphoid malignancies and associated with Akt

AUTHOR(S): Favaro, Patricia M. Bergamo; Medina, Samuel de Souza; Traina, Fabiola; Basseres, Daniela Sanchez; Costa, Fernando Ferreira; Saad, Sara Teresinha Olalla
CORPORATE SOURCE: Centro de Hematologia e Hemoterapia, Universidade Estadual de Campinas, Campinas, 13083-970, Brazil
SOURCE: Biochemical and Biophysical Research Communications (2003), 311(2), 365-371
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Elsevier Science
DOCUMENT TYPE: Journal
LANGUAGE: English
AB The very large family of **Formin** proteins is involved in processes such as morphogenesis, embryonic differentiation, cell polarity, and cytokinesis. A novel human gene from the **Formin** family, designated human leukocyte **formin** gene, was cloned. The cDNA of the gene was determined to be 3959 bp long with an open reading frame of 3302 bp and computational anal. located this gene on chromosome 17, suggesting that it is composed of 27 exons. Northern blot anal. revealed a restricted expression of mRNA in the thymus, **spleen**, and peripheral blood leukocytes in normal human tissues. Western blot anal. demonstrated that the protein encoded by this gene is overexpressed in lymphoid malignancies; cancer cell lines and peripheral blood leukocyte from chronic lymphocytic leukemia (CLL) patients. Furthermore, the human leukocyte **formin** protein was observed to associate with Akt, a critical survival regulator in many different cell types.
REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 2 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:968465 HCAPLUS
DOCUMENT NUMBER: 139:169252
TITLE: Evaluation of irrigation effects of NaOCl and H2O2 on mice spleen lymphocytes: a novel in vitro model
AUTHOR(S): Yamaguchi, H.; Fujihashi, K.; Arai, T.; Cox, C. F.
CORPORATE SOURCE: Departments of Comprehensive Dentistry, and Endodontics & Pulp Biology, The University of Alabama at Birmingham School of Dentistry, USA
SOURCE: Dentin/Pulp Complex, Proceedings of the International Conference on Dentin/Pulp Complex, 4th, Chiba, Japan, 2001 (2002), Meeting Date 2001, 128-129. Editor(s): Ishikawa, Tatsuya. Quintessence Publishing Co., Ltd.: Tokyo, Japan.
CODEN: 69DJTU; ISBN: 4-87417-733-6
DOCUMENT TYPE: Conference
LANGUAGE: English
AB Recent studies have reported high success rates following mech. pulp exposure and direct capping with various adhesive systems, and histol. studies have demonstrated that NaOCl produces a surface amputation of the subjacent pulp interface without causing damage to the deeper pulp tissue. However, the results of these studies did not make clear any damage to the lymphocytes of the underlying exposed pulp. The present study evaluated whether specific concns. of H2O2 and/or NaOCl would cause measurable damage to extracted mice spleen lymphocytes using a modified microtube as an exposed pulp model. Mice spleen lymphocyte surface cells were reduced with high concns. of NaOCl. This study suggests that treatment of pulp tissues with high concns. of either NaOCl or H2O2 may adversely affect normal tissues. This in vitro microtube using mice spleen lymphocytes is a simplified model to study an exposed pulp.
IT **7681-52-9**, Sodium hypochlorite
RL: ADV (Adverse effect, including toxicity); THU (Therapeutic use); BIOL

(Biological study); USES (Uses)
(a novel in vitro model for evaluation of irrigation effects of NaOCl and H2O2 on mice **spleen** lymphocytes)
RN 7681-52-9 HCAPLUS
CN Hypochlorous acid, sodium salt (8CI, 9CI) (CA INDEX NAME)



REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 3 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2000:642522 HCAPLUS
DOCUMENT NUMBER: 133:332798
TITLE: FRL, a novel formin-related protein, binds to Rac and regulates cell motility and survival of macrophages
AUTHOR(S): Yayoshi-Yamamoto, Shinri; Taniuchi, Ichiro; Watanabe, Takeshi
CORPORATE SOURCE: Department of Molecular Immunology, Medical Institute of Bioregulation, Kyushu University, Fukuoka, 812-8582, Japan
SOURCE: Molecular and Cellular Biology (2000), 20(18), 6872-6881
CODEN: MCEBD4; ISSN: 0270-7306
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB We have isolated a cDNA, frl (**formin**-related gene in leukocytes), a novel mammalian member of the **formin** gene family. The frl cDNA encodes a 160-kDa protein, FRL, that possesses FH1, FH2, and FH3 domains that are well conserved among other **Formin**-related proteins. An FRL protein is mainly localized in the cytosol and is highly expressed in **spleen**, lymph node, and bone marrow cells. **Formin**-related genes and proteins have been reported to play crucial roles in morphogenesis, cell polarity, and cytokinesis through interaction with Rho family small GTPases. FRL binds to Rac at its N-terminal region including the FH3 domain and assocs. with profilin at the FH1 domain. In a macrophage cell line, P388D1, overexpression of a truncated form of FRL containing only the FH3 domain (FH3-FRL) strongly inhibited cell adhesion to fibronectin and migration upon stimulation with a chemokine. Moreover, expression of the truncated FH3-FRL protein resulted in apoptotic cell death of P388D1 cells, suggesting that the truncated FH3-FRL protein may interfere with signals of FRL. Overexpression in the P388D1 cells of full-length FRL or of the truncated protein containing the FH3 and FH1 domains, with simultaneous expression of the truncated FH3-FRL protein, blocked apoptotic cell death and inhibition of cell adhesion and migration. These results suggest that FRL may play a role in the control of reorganization of the actin cytoskeleton in association with Rac and also in the regulation of the signal for cell survival.
REFERENCE COUNT: 57 THERE ARE 57 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L11 ANSWER 4 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1981:562089 HCAPLUS

DOCUMENT NUMBER: 95:162089
TITLE: Effect of phenformin, L-DOPA and p-chlorophenylalanine treatment on the immune response and chemical carcinogenesis development in BALB/c mice
AUTHOR(S): Vinnitskii, V. B.; Yakimenko, V. A.
CORPORATE SOURCE: R. E. Kavetskii Inst. Oncol., Kiev, USSR
SOURCE: Voprosy Onkologii (1981), 27(6), 45-50
CODEN: VOONAW; ISSN: 0507-3758
DOCUMENT TYPE: Journal
LANGUAGE: Russian
AB Mice receiving 20-methylcholanthrene [56-49-5] showed hypothalamic dopamine [51-61-6], noradrenaline [51-41-2], and serotonin [50-67-9] at 0.81, 2.74, and 2.05 μg/g, compared with 0.78, 1.79, and 1.66 μg/g, resp., for intact mice. The resp. values for mice immunized with sheep erythrocytes were 0.79, 0.97, and 1.88 μg/g, and for mice receiving both 20-methylcholanthrene and sheep erythrocytes, 0.77, 3.1, and 1.93 μg/g. Normalization of hypothalamic neuromediators in carcinogen-treated mice by phenformin **[114-86-3]**, p-chlorophenylalanine [1991-78-2], and dopa [59-92-7] led to greater nos. of **spleen** antibody-forming cells upon immunization with sheep erythrocytes and potentiated the inhibiting action of immunostimulators (zymosans, BCG vaccine) on the tumor.

L11 ANSWER 5 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1975:119820 HCAPLUS
DOCUMENT NUMBER: 82:119820
TITLE: Poisoning of animals by mercury preparations
AUTHOR(S): Arestov, I. G.; Antyukov, M. A.
CORPORATE SOURCE: Vitebsk. Vet. Inst., Vitebsk, USSR
SOURCE: Veterinariya (Moscow, Russian Federation) (1974), (11), 109-10
CODEN: VETNAL; ISSN: 0042-4846
DOCUMENT TYPE: Journal
LANGUAGE: Russian
AB Hemorrhagic gastroenteritis, ulcers of the small intestine mucosa, focal hemorrhages in the **spleen** and kidneys, and liver dystrophy were detected in cattle poisoned by rye seeds treated with Granosan [107-27-7]. When applied at 40 g/specimen against ectoparasites, an ointment containing Hg [7439-97-6] also caused toxic effects. I.v. injections of glucose [50-99-7], CaCl2 [10043-52-4], antibiotics, vitamins, i.m. injections of unithiol [4076-02-2], and s.c. injections of cardiamine [**59-26-7**] had significant therapeutic effects.

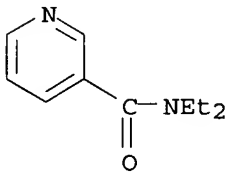
L11 ANSWER 6 OF 6 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1963:10912 HCAPLUS
DOCUMENT NUMBER: 58:10912
ORIGINAL REFERENCE NO.: 58:1835f-h
TITLE: The influence of nikethamide and cardiazol on certain chemoreceptors
AUTHOR(S): Wang, I-Ming
CORPORATE SOURCE: Shanghai Med. Coll.
SOURCE: Sheng Li Huseh Pao (1959), 23, 105-13
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB The stimulating effects of nikethamide (I) and cardiazol (II) on the chemoreceptors of the carotid body, spleen, intestine, and bone marrow of the tibia were studied in cats, with reflex changes in respiration and arterial blood pressure as indicators. I(0.2-0.4 ml. of 5% solution) introduced into the perfusate entering the carotid sinus produced momentary respiratory inhibition. When 0.1-0.2 ml. of 25% I was

introduced, momentary inhibition, apnea, or mild stimulation after inhibition was observed. Similar results were obtained with II. I or II (0.2-0.5 ml. of 1-5% solution) introduced into the perfusate entering the spleen and intestinal loop stimulated their chemoreceptors and evoked respiratory excitation and a rise of arterial blood pressure. I or II (0.1 mol. of 0.1-0.2% solution) instilled into the bone marrow of the tibia through drilled openings produced respiratory stimulation and a rise of blood pressure. The excitatory effects of these drugs on the chemoreceptors described could be abolished by previous application of procaine but they reappeared when the action of procaine was over. From the above, it may be concluded that I, like II, has little stimulating action on the carotid chemoreceptors, but they stimulate the chemoreceptors of the spleen, intestine, and bone marrow and cause a reflex rise of the arterial blood pressure and augmentation of respiration.

IT **59-26-7**, Nicotinamide, N,N-diethyl-
(chemoreceptors in bone marrow, carotid body, intestine and **spleen** in relation to)

RN 59-26-7 HCAPLUS

CN 3-Pyridinecarboxamide, N,N-diethyl- (9CI) (CA INDEX NAME)



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                 ESIS? OR ?GLYCEM?)
L6           796 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L4(L)(MRNA OR DNA OR ?NUCLE?
                 OR PROTEIN)
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L10           11 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L4(L)SPLEEN
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L12          183 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L4(L)GENE
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L16           85 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L15 NOT (L2 OR L8 OR L11 OR
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L17           22 SEA FILE=HCAPLUS ABB=ON  PLU=ON  L16 AND (L4 OR ?DIABET? OR
                 INSULIN? OR ?GLYCEM? OR SPLEEN OR MRNA OR DNA OR ?NUCLE? OR
                 PROTEIN OR GENE)


=> d ibib abs l17 1-22

L17  ANSWER 1 OF 22  HCAPLUS  COPYRIGHT 2005 ACS on STN
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ACCESSION NUMBER: 2005:495285 HCAPLUS
DOCUMENT NUMBER: 143:110010
TITLE: P115 interacts with the GLUT4 vesicle **protein**, IRAP, and plays a critical role in **insulin**-stimulated GLUT4 translocation
AUTHOR(S): Hosaka, Toshio; **Brooks, Cydney C.**; Presman, Eleonora; Kim, Suk-Kyeong; Zhang, Zidong; Breen, Michael; Gross, Danielle N.; Sztul, Elizabeth; Pilch, Paul F.
CORPORATE SOURCE: Department of Biochemistry, Boston University School of Medicine, Boston, MA, 02118, USA
SOURCE: Molecular Biology of the Cell (2005), 16(6), 2882-2890
CODEN: MBCEEV; ISSN: 1059-1524
PUBLISHER: American Society for Cell Biology
DOCUMENT TYPE: Journal
LANGUAGE: English

AB **Insulin**-regulated aminopeptidase (IRAP) is an abundant cargo **protein** of Glut4 storage vesicles (GSVs) that traffics to and from the plasma membrane in response to **insulin.** We used the amino terminus cytoplasmic domain of IRAP, residues 1-109, as an affinity reagent to identify cytosolic **proteins** that might be involved in GSV trafficking. In this way, we identified p115, a peripheral membrane **protein** known to be involved in membrane trafficking. In murine adipocytes, we determined that p115 was localized to the **perinuclear** region by immunofluorescence and throughout the cell by fractionation. By immunofluorescence, p115 partially colocalizes with GLUT4 and IRAP in the **perinuclear** region of cultured fat cells. The amino terminus of p115 binds to IRAP and overexpression of a N-terminal construct results in its colocalization with GLUT4 throughout the cell. **Insulin**-stimulated GLUT4 translocation is completely inhibited under these conditions. Overexpression of p115 C-terminus has no significant effect on GLUT4 distribution and translocation. Finally, expression of the p115 N-terminus construct has no effect on the distribution and trafficking of GLUT1. These data suggest that p115 has an important and specific role in **insulin**-stimulated Glut4 translocation, probably by way of tethering **insulin**-sensitive Glut4 vesicles at an as yet unknown intracellular site.

REFERENCE COUNT: 48 THERE ARE 48 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 2 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2005:59907 HCAPLUS
DOCUMENT NUMBER: 142:148800
TITLE: Use of **insulin** response modulators in the treatment of **diabetes** and **insulin** resistance
INVENTOR(S): **Brooks, Cydney C.**
PATENT ASSIGNEE(S): Adipogenix, Inc., USA
SOURCE: U.S. Pat. Appl. Publ., 37 pp., Cont.-in-part of Appl. No. PCT/US02/14493.
CODEN: USXXCO
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2005014194	A1	20050120	US 2003-627311	20030725
WO 2002090932	A2	20021114	WO 2002-US14493	20020508

WO 2002090932 A3 20040521
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2001-289669P P 20010508
WO 2002-US14493 A2 20020508
US 2002-406618P P 20020827

AB Methods of identifying **insulin** response modulators are provided. Therapeutic methods utilizing compds. identified according to the methods of the invention are also provided. In particular, methods of treating **diabetes** and **insulin** resistance are provided.

L17 ANSWER 3 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:889010 HCAPLUS
DOCUMENT NUMBER: 137:379963
TITLE: Methods and reagents for identifying **insulin** response modulators and therapeutic uses therefor
INVENTOR(S): **Brooks, Cydney C.**
PATENT ASSIGNEE(S): Adipogenix, Inc., USA; Takeda Chemical Industries, Ltd.
SOURCE: PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002093128	A2	20021121	WO 2002-US15208	20020513
WO 2002093128	A3	20030626		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG
PRIORITY APPLN. INFO.: US 2001-290602P P 20010511

AB Methods of identifying **insulin** response modulators are provided. In particular, methods that feature identifying modulators of **insulin**-responsive aminopeptidase (IRAP) and IRAP-binding **protein**-2 (IRAP-BP-2), or activities associated therewith, are provided. Therapeutic methods utilizing compds. identified according to the methods of the invention are also provided.

L17 ANSWER 4 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:889009 HCAPLUS
DOCUMENT NUMBER: 137:379962
TITLE: Methods and reagents for identifying **insulin**

response modulators and therapeutic uses therefor
INVENTOR(S): **Brooks, Cydney C.**
PATENT ASSIGNEE(S): Adipogenix, Inc., USA; Takeda Chemical Industries, Ltd.
SOURCE: PCT Int. Appl., 40 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002093127	A2	20021121	WO 2002-US15206	20020513
WO 2002093127	A3	20040923		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
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PRIORITY APPLN. INFO.: US 2001-290494P P 20010511

AB Methods of identifying **insulin** response modulators are provided. In particular, methods that feature identifying modulators of **insulin**-responsive aminopeptidase (IRAP) and **insulin** -degrading enzyme (IDE), or activities associated therewith, are provided. Therapeutic methods utilizing compds. identified according to the methods of the invention are also provided.

L17 ANSWER 5 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:869182 HCAPLUS
DOCUMENT NUMBER: 137:363027
TITLE: Methods and reagents for identifying **insulin** response modulators and therapeutic uses therefor
INVENTOR(S): **Brooks, Cydney C.**
PATENT ASSIGNEE(S): Adipogenix, Inc., USA; Takeda Chemical Industries, Ltd.
SOURCE: PCT Int. Appl., 51 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 2
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002090932	A2	20021114	WO 2002-US14493	20020508
WO 2002090932	A3	20040521		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW
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GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG

US 2005014194 A1 20050120 US 2003-627311 20030725
PRIORITY APPLN. INFO.: US 2001-289669P P 20010508
WO 2002-US14493 A2 20020508
US 2002-406618P P 20020827

AB The invention features methods of identifying **insulin** response modulators, in particular, methods that involve transcytosis-associated **protein** (TAP) and **insulin**-responsive aminopeptidase binding **protein** (IRAP) polypeptide reagents and/or cells that overexpress TAP. In particular, the methods (e.g., cell free and/or cell-based methods) feature determining the ability of a test compound to effect the interaction of TAP, or a bioactive fragment thereof, with IRAP or a bioactive fragment thereof, the ability to effect such an interaction being determinative of the compound's ability to modulate **insulin** responsive GLUT4 translocation and, ultimately, glucose uptake. Reagents, for example, polypeptide reagents and cellular reagents, fusion **proteins**, antibodies and the like are also featured. Other aspect of the invention feature modulators identified by the methods described herein as well as therapeutic methods for modulating **insulin** responsiveness using such modulators.

L17 ANSWER 6 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2002:328640 HCAPLUS
DOCUMENT NUMBER: 137:215187
TITLE: No evidence of mutations in the CACNA1S **gene** in the UK malignant hyperthermia population
AUTHOR(S): **Brooks, C.**; Robinson, R. L.; Halsall, P. J.; Hopkins, P. M.
CORPORATE SOURCE: MH Investigation Unit, St James' University Hospital, Leeds, LS9 7TF, UK
SOURCE: British Journal of Anaesthesia (2002), 88(4), 587-589
CODEN: BJANAD; ISSN: 0007-0912
PUBLISHER: Oxford University Press
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Malignant hyperthermia (MH) is an inherited, potentially fatal, pharmacogenetic disorder triggered by certain anesthetic agents. In light of the reported genetic heterogeneity for the disorder and the recent introduction of **DNA** testing guidelines for the trait, the authors have assessed the role of the CACNA1S **gene** in MH susceptibility in UK patients. Linkage to this locus has previously been demonstrated in several European MH families. The authors screened 200 unrelated MH-susceptible individuals for known CACNA1S mutations. With the aim to characterize further novel mutations at this locus, functionally relevant regions of the **gene** were also sequenced in 10 unrelated individuals from families where the involvement of other MH susceptibility loci was unlikely. No sequence variations were detected in any of the patients investigated. Defects in CACNA1S are not a major cause of MH in the UK population. Diagnostic screening of this **gene** is unlikely to be of value to UK MH patients in the near future.

REFERENCE COUNT: 10 THERE ARE 10 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 7 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 2000:81213 HCAPLUS
DOCUMENT NUMBER: 132:204410
TITLE: Pantophysin is a phosphoprotein component of adipocyte

transport vesicles and associates with GLUT4-containing vesicles

AUTHOR(S): **Brooks, Cydney C.**; Scherer, Philipp E.; Cleveland, Kelly; Whittemore, Jennifer L.; Lodish, Harvey F.; Cheatham, Bentley

CORPORATE SOURCE: Research Division, Joslin Diabetes Center and Department of Medicine, Harvard Medical School, Boston, MA, 02215, USA

SOURCE: Journal of Biological Chemistry (2000), 275(3), 2029-2036
CODEN: JBCHA3; ISSN: 0021-9258

PUBLISHER: American Society for Biochemistry and Molecular Biology

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Pantophysin, a **protein** related to the neuroendocrine-specific synaptophysin, recently has been identified in non-neuronal tissues. In the present study, Northern blots showed that pantophysin **mRNA** was abundant in adipose tissue and increased during adipogenesis of 3T3-L1 cells. Immunoblot anal. of subcellular fractions showed pantophysin present exclusively in membrane fractions and relatively evently distributed in the plasma membrane and internal membrane fractions. Sucrose gradient ultracentrifugation demonstrated that pantophysin and GLUT4 exhibited overlapping distribution profiles. Furthermore, immunopurified GLUT4 vesicles contained pantophysin, and both GLUT4 and pantophysin were depleted from this vesicle population following treatment with **insulin**. Addnl., a subpopulation of immunopurified pantophysin vesicles contained **insulin**-responsive GLUT4. Consistent with the interaction of synaptophysin with vesicle-associated membrane **protein** 2 in neuroendocrine tissues, pantophysin associated with vesicle-associated membrane **protein** 2 in adipocytes. Furthermore, in [32P]orthophosphate-labeled cells, pantophysin was phosphorylated in the basal state. This phosphorylation was unchanged in response to **insulin**; however, **insulin** stimulated the phosphorylation of a 77-kDa **protein** associated with α-pantophysin immunoppts. Although the functional role of pantophysin in vesicle trafficking is unclear, its presence on GLUT4 vesicles is consistent with the emerging role of soluble N-ethylmaleimide-sensitive **protein** receptor (SNARE) factor complex and related **proteins** in regulated vesicle transport in adipocytes. In addition, pantophysin may provide a marker for the anal. of other vesicles in adipocytes.

REFERENCE COUNT: 56 THERE ARE 56 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L17 ANSWER 8 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN

ACCESSION NUMBER: 1994:695708 HCAPLUS

DOCUMENT NUMBER: 121:295708

TITLE: Purification and Biochemical Characterization of Recombinant N-Methylpurine-**DNA** Glycosylase of the Mouse

AUTHOR(S): Roy, R.; **Brooks, C.**; Mitra, S.

CORPORATE SOURCE: Sealy Center for Molecular Science, University of Texas, Galveston, TX, 77555, USA

SOURCE: Biochemistry (1994), 33(50), 15131-40
CODEN: BICHAW; ISSN: 0006-2960

DOCUMENT TYPE: Journal

LANGUAGE: English

AB The mouse N-methylpurine-**DNA** glycosylase (MPG), responsible for the removal of most N-alkyladducts in **DNA**, was purified to

homogeneity as a recombinant nonfusion **protein** from Escherichia coli. Only 10-15% of the **protein** was present in the soluble form in E. coli cells. The N-terminal amino acid sequence of the purified **protein** which lacks 48 residues from the amino terminus of the wild type **protein** was identical to that predicted from the **nucleotide** sequence. The glycosylase hydrolyzes 3-methyladenine (m3A), 7-methylguanine (m7G), and 3-methylguanine (m3G) from **DNA** , and the Km and kcat values were 130 nM and 0.8 min-1 for m3A, and 860 nM and 0.2 min-1 for m7G, resp., when methylated calf thymus **DNA** was used as the substrate. A comparison of kcat/Km values for different bases indicates that the enzyme was more efficient in excising both m3A and m3G than m7G from methylated **DNA.** The enzyme showed moderate binding affinities (KA) for both methylated (5.8 + 107 M-1) and nonmethylated **DNAs** (4.2 + 107 M-1). The mouse **protein** has an extinction coefficient E1%280nm of 10.5 and a pI of 9.3. The enzyme activity was optimal in the presence of 100 mM NaCl, with a broad pH optimum of 8.5-9.5. The enzymic release of both m3A and m7G was stimulated 50-75% by 0.5 mM MgCl2 and 0.02 mM spermine but inhibited by higher concns. of these agents. Product inhibition by 40-50% of the reaction occurred in the presence of 10 mM m3A or m7G. However, 1.0 mM m3A stimulated release of m7G. The enzyme was inhibited by 60% in the presence of 0.9 mg/mL **DNA** which, at the same time, protected it from thermal inactivation.

L17 ANSWER 9 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1994:267426 HCAPLUS
DOCUMENT NUMBER: 120:267426
TITLE: Identification and characterization of aldolase B mutations in American patients with hereditary fructose in tolerance
AUTHOR(S): **Brooks, Cydney Carolyn**
CORPORATE SOURCE: Boston Univ., Boston, MA, USA
SOURCE: (1994) 162 pp. Avail.: Univ. Microfilms Int., Order No. DA9322298
From: Diss. Abstr. Int. B 1993, 54(3), 1227
DOCUMENT TYPE: Dissertation
LANGUAGE: English
AB Unavailable

L17 ANSWER 10 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1994:160768 HCAPLUS
DOCUMENT NUMBER: 120:160768
TITLE: A partially active mutant aldolase B from a patient with hereditary fructose intolerance
AUTHOR(S): **Brooks, Cydney C.**; Tolan, Dean R.
CORPORATE SOURCE: Biol. Dep., Boston Univ., Boston, MA, 02215, USA
SOURCE: FASEB Journal (1994), 8(1), 107-13
CODEN: FAJOEC; ISSN: 0892-6638
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Hereditary fructose intolerance (HFI) is a potentially fatal autosomal recessive disease of carbohydrate metabolism HFI patients are deficient in aldolase B, the isoenzyme expressed in fructose-metabolizing tissues. The eight **protein** coding exons, including splicing signals, of the aldolase B **gene** from one American HFI patient were amplified by the polymerase chain reaction (PCR). Single-strand conformational polymorphism (SSCP) anal. and direct sequence determination were applied to the amplified fragments. The mutations in the patient's alleles were identified as a nonsense mutation (R59op) in exon 3 and a missense mutation (C134R) in exon 5. These mutations were confirmed by sequence

determination of cloned PCR-amplified exons 3 and 5 from the patient. Allele specific **oligonucleotide** (ASO) hybridizations of amplified exons 3 and 5 showed the Mendelian inheritance of both mutations. Site-directed mutagenesis was used to generate an expression plasmid for the C134R mutation, and the mutant enzyme was expressed in bacteria. Assays of partially purified enzyme prepns. showed that this missense mutation results in an apparently unstable enzyme that retains partial activity. This is the first evidence for a partially active aldolase B from an HFI individual with an identified mutation, and supports the hypothesis that adequate gluconeogenesis/glycolysis is maintained in HFI patients by the presence of partially active enzymes.

L17 ANSWER 11 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1994:104049 HCAPLUS
DOCUMENT NUMBER: 120:104049
TITLE: Association of the widespread A149P hereditary fructose intolerance mutation with newly identified sequence polymorphisms in the aldolase B **gene**
AUTHOR(S): **Brooks, Cydney C.**; Tolan, Dean R.
CORPORATE SOURCE: Dep. Biol., Boston Univ., Boston, MA, USA
SOURCE: American Journal of Human Genetics (1993), 52(4), 835-840
CODEN: AJHGAG; ISSN: 0002-9297
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Hereditary fructose intolerance (HFI) is a potentially fatal autosomal recessive disease resulting from the catalytic deficiency of fructose 1-phosphate aldolase (aldolase B) in fructose-metabolizing tissues. The A149P mutation in exon 5 of the aldolase B **gene**, located on chromosome 9q21.3-q22.2, is widespread and the most common HFI mutation, accounting for 57% of HFI chromosomes. The possible origin of this mutation was studied by linkage to polymorphisms within the aldolase B **gene**. **DNA** fragments of the aldolase B **gene** containing the polymorphic marker loci from HFI patients homozygous for the A149P allele were amplified by PCR. Absolute linkage to a common PvuII RFLP allele was observed in 10 A149P homozygotes. In a more informative study, highly heterozygous polymorphisms were detected by direct sequence determination of a PCR-amplified aldolase B **gene** fragment. Two two-allele, single-base-pair polymorphisms, themselves in absolute linkage disequil., in intron 8 (C at **nucleotide** 84 and A at **nucleotide** 105, or T at 84 and G at 105) of the aldolase B **gene** were identified. Mendelian segregation of these polymorphisms was confirmed in three families. Allele-specific **oligonucleotide** (ASO) hybridizations with probes for both sequence polymorphisms showed that 47% of 32 unrelated individuals were heterozygous at these loci; the calculated PIC value was .37. Finally, ASO hybridizations of PCR-amplified **DNA** from 15 HFI patients homozygous for the A149P allele with probes for these sequence polymorphisms revealed absolute linkage disequil. between the A149P mutation and the 84T/105G allele. These results are consistent with a single origin of the A149P allele and subsequent spread by genetic drift.

L17 ANSWER 12 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1992:631608 HCAPLUS
DOCUMENT NUMBER: 117:231608
TITLE: Molecular analysis of common aldolase B alleles for hereditary fructose intolerance in North Americans
AUTHOR(S): Tolan, Dean R.; **Brooks, Cydney C.**
CORPORATE SOURCE: Biol. Dep., Boston Univ., Boston, MA, 02215, USA
SOURCE: Biochemical Medicine and Metabolic Biology (1992),

48(1), 18-25
CODEN: BMMBES; ISSN: 0885-4505
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The diagnosis of hereditary fructose intolerance (HFI) presents a difficult challenge that often involves procedures of high risk to the patient. A relatively noninvasive method that involves mol. anal. of common alleles would offer a decided advantage. The mol. defects in the aldolase B **gene** were studied in 31 HFI subjects (23 pedigrees, 47 apparently independent alleles) from the United States and Canada. The authors screened for the 3 most common European alleles by direct hybridization of allele-specific **oligodeoxyribonucleotides** (ASOs) to portions of the aldolase B **gene** that were amplified by PCR. Fifty-five percent of mutant North American alleles were A149P (Ala149 → Pro), the most common mutation in the European population. The other two alleles, A174D (Ala174 → Asp) and N334K (Asn334 → Lys), represent 11 and 2% of North American alleles, resp. Nine patients, representing 32% of independent alleles studied, had an HFI allele that was not of this common missense class. This North American allele distribution is different from that in Europe, where 13% of HFI alleles are not of this type. Preliminary screening of amplified **DNA** with this set of ASOs indicated that 80% of symptomatic HFI patients can be identified in the American population by this simple genetic test.

L17 ANSWER 13 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1992:126210 HCAPLUS
DOCUMENT NUMBER: 116:126210
TITLE: Identification of a splice-site mutation in the aldolase B **gene** from an individual with hereditary fructose intolerance
AUTHOR(S): **Brooks, Cydney C.**; Buist, Neil; Tuerck, Judith; Tolan, Dean R.
CORPORATE SOURCE: Dep. Biol., Boston Univ., Boston, MA, 02215, USA
SOURCE: American Journal of Human Genetics (1991), 49(5), 1075-81
CODEN: AJHGAG; ISSN: 0002-9297
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Hereditary fructose intolerance (HFI) is a potentially fatal autosomal recessive disease of carbohydrate metabolism HFI patients exhibit a deficiency of fructose 1-phosphate aldolase (aldolase B), the isoenzyme expressed in tissues that metabolize fructose. The 8 **protein** -coding exons, including splicing signals, of the aldolase B **gene** from one HFI patient were amplified by PCR. Dot-blot hybridization of the amplified **DNA** with allele-specific **oligonucleotide** (ASO) probes revealed a previously described A149P mutation in 1 allele from the proband. The mutation in the other allele was identified by direct sequencing of the double-stranded PCR-amplified material from the proband. The **nucleotide** sequence of exon 9 revealed a 7-base deletion/1-base insertion (Δ7 + 1) at the 3' splice site of intron 8 in one allele. This mutation was confirmed by cloning PCR-amplified exon 9 of the proband and determining the sequence of each allele sep. ASO anal. of 18 family members confirmed the Mendelian inheritance of both mutant alleles. The implications of this unique splice-site mutation in HFI are discussed.

L17 ANSWER 14 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1973:430756 HCAPLUS
DOCUMENT NUMBER: 79:30756

TITLE: Effect of methionine, pig weight, sex, and diet on digestion
AUTHOR(S): Huck, D. W.; **Brooks, C. C.**
CORPORATE SOURCE: Univ. Hawaii, Honolulu, HI, USA
SOURCE: Proceedings, Annual Meeting - American Society of Animal Science, Western Section (1972), 23, 118-21
CODEN: PMWSA7; ISSN: 0569-7832
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The digestibility effect of 0.15% methionine supplementation to a 15% sucrose (65%)-soybean meal (31%) and a 19% corn (77%)-soybean meal (20%) diet fed to pigs was investigated. Methionine increased digestibility in the light-weight pigs but depressed it in the heavy pigs. Sugar-based diets were more digestible than corn-based diets among the light-weight pigs. Heavy-weight gilts were more efficient in digestion than heavy-weight barrows. Digestibility of the corn-based diets increased with weight of the pigs, but only **protein** digestibility of the sugar-based diets increased with weight

L17 ANSWER 15 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1972:33098 HCAPLUS
DOCUMENT NUMBER: 76:33098
TITLE: Effect of coconut meal on Corturnix quail and of coconut meal and coconut oil on performance, carcass measurements, and fat composition in swine
AUTHOR(S): Creswell, D. C.; **Brooks, C. C.**
CORPORATE SOURCE: Univ. Hawaii, Honolulu, HI, USA
SOURCE: Journal of Animal Science (Savoy, IL, United States) (1971), 33(2), 370-5
CODEN: JANSAG; ISSN: 0021-8812
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Pig gains and feed efficiency decreased as the level of coconut meal in the diet was increased from 0 to 40%. Loin eye area and ham weight also decreased. These decreases in gain and muscle development were not overcome by increasing **protein** or lysine levels. Inclusion of 40% coconut meal in corn-based diet rations (at the expense of corn and soybean meal) increased gains in quail, and addition of 0.36% L-lysine.HCl resulted in further increases. Coconut meal decreased the percent of stearic acid in the backfat of pigs; coconut oil decreased that of oleic acid.

L17 ANSWER 16 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1972:2768 HCAPLUS
DOCUMENT NUMBER: 76:2768
TITLE: Composition, apparent digestibility, and energy evaluation of coconut oil and coconut meal
AUTHOR(S): Creswell, D. C.; **Brooks, C. C.**
CORPORATE SOURCE: Univ. Hawaii, Honolulu, HI, USA
SOURCE: Journal of Animal Science (Savoy, IL, United States) (1971), 33(2), 366-9
CODEN: JANSAG; ISSN: 0021-8812
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The addition of >10 coconut meal to swine feed caused a decrease in **protein** and dry matter digestibility. **Protein** in coconut meal had an apparent digestibility of 50.7. The digestible energy content of coconut meal-containing diets was 3.6 kcal/g. Digestion coeffs. for **protein** and ether extract were greater when diets contained 10 coconut oil. In addition to proximate anal., data on the content of Ca, P,

Mg, K, Zn, Cu, and Mn in coconut meal were obtained.

L17 ANSWER 17 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1971:516256 HCAPLUS
DOCUMENT NUMBER: 75:116256
TITLE: Sucrose-induced hemorrhagic syndrome in swine
AUTHOR(S): Nakamura, R. M.; **Brooks, C. C.**; Miyahara, A. Y.
CORPORATE SOURCE: Univ. Hawaii, Honolulu, HI, USA
SOURCE: Proceedings, Annual Meeting - American Society of Animal Science, Western Section (1971), 22, 239-43
CODEN: PMWSA7; ISSN: 0569-7832
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Feeding a high-sucrose-soybean meal ration markedly increased the prothrombin time and thromboplastin in 3 of 5 pigs. An inexplicable decrease in clotting time was detected in 1 of the 3 pigs prior to menadione supplementation, which ameliorated the clin. observed signs of lethargy and lameness. The 2 pigs that died during high-sucrose feeding had massive internal hemorrhages; 1 also had hemorrhages in the joints and diaphragm. Gross lesions were not seen in the 3 pigs killed at the end of the experiment Heart lesions were not seen in any of the 5 pigs. Hematol. studies did not show detectable changes in nos. of red and white blood cells, or in differential white blood cell counts, and packed cell volume and Hb levels were not affected. Increases in serum **protein** levels were detectable after high-sucrose feeding, and were not affected by menadione supplementation.

L17 ANSWER 18 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1962:75459 HCAPLUS
DOCUMENT NUMBER: 56:75459
ORIGINAL REFERENCE NO.: 56:14710h-i
TITLE: Influence of trace mineral, **protein** source, and method of feeding on growth rate, **protein** intake, and **protein** needs by growing swine
AUTHOR(S): **Brooks, C. C.**; Thomas, H. R.
CORPORATE SOURCE: Virginia Polytech. Inst., Blacksburg
SOURCE: Virginia Agr. Expt. Sta. Tech. Bull. (1958), No. 138, 8 pp.
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB The influence of trace minerals (Mn 0.2, Fe 0.16, Cu 0.01, I 0.007% in salt mixture), **protein** source, and method of feeding on growth rate, **protein** intake, and **protein** needs of growing swine were investigated. Weanling pigs were treated for internal parasites, vaccinated against cholera, and placed in concrete pens. In the 1st test, pigs did not balance rations when fed ad libitum. When fed ad libitum, trace minerals caused a 0.2-0.6 lb. increase/day in **protein** intake, but did not increase rate of gain or feed efficiency. **Protein** supplements were effective in the following decreasing order: mixed **protein**, soybean oil meal, peanut oil meal. The 2nd test indicated that trace minerals did not improve practical rations, nor did they influence **protein** need.

L17 ANSWER 19 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1958:21776 HCAPLUS
DOCUMENT NUMBER: 52:21776
ORIGINAL REFERENCE NO.: 52:3956i,3957a-b
TITLE: Effects of steroid and steroid-like compounds on digestion of rations by ruminants. In vivo and in

vitro studies using diethylstilbestrol, cholesterol, estrone, testosterone, cortisone, and hexestrol
AUTHOR(S): Pfander, W. H.; Kelley, R. W.; **Brooks, C. C.** ; Gehrke, C. W.; Muhrer, M. E.
CORPORATE SOURCE: Univ. of Missouri, Columbia
SOURCE: Missouri Univ., Agr. Expt. Sta. Research Bull. (1957), No. 632, 15 pp.
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB By use of the artificial rumen technique it was found that digestion of cellulose is improved by the addition of diethylstilbestrol (2-20 p.p.m.), cholesterol (20 p.p.m.), estrone (20 p.p.m.), testosterone (10 p.p.m.), and cortisone (25 p.p.m.). Hexestrol depressed cellulose digestion slightly. Ten or 20 p.p.m. of stilbestrol, added to cottonseed hull-casein ration, increased the digestibility of cellulose and **protein**, but sheep could not tolerate the dosages used. Hexestrol had no effect on the digestibility of silage rations by steer calves. It is concluded that, in general, the steroid-like compds. influence the cellulolytic activity of rumen microflora.

L17 ANSWER 20 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1955:20659 HCAPLUS
DOCUMENT NUMBER: 49:20659
ORIGINAL REFERENCE NO.: 49:4099e-f
TITLE: The effect of added fat on the digestion of cellulose and **protein** by ovine rumen microorganisms
AUTHOR(S): **Brooks, C. C.**; Garner, G. B.; Gehrke, C. W.; Muhrer, M. E.; Pfander, W. H.
CORPORATE SOURCE: Univ. of Missouri, Columbia
SOURCE: Journal of Animal Science (Savoy, IL, United States) (1954), 13, 758-64
CODEN: JANSAG; ISSN: 0021-8812
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB The addition of corn oil (10-170 mg.) to a g. of dry matter (50% cellulose) significantly reduced cellulose digestion in the artificial rumen inoculated with ovine rumen organisms. The addition of 32 or 64 g. of corn oil or lard to a basal ration of cottonseed hulls and casein reduced cellulose and **protein** digestion in sheep. The depressing effects of corn oil were partially overcome by the addition of alfalfa ash.

L17 ANSWER 21 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1955:12776 HCAPLUS
DOCUMENT NUMBER: 49:12776
ORIGINAL REFERENCE NO.: 49:2584a-c
TITLE: Effect of steroid compounds on ovine rumen function
AUTHOR(S): **Brooks, C. C.**; Garner, G. B.; Muhrer, M. E.; Pfander, W. H.
CORPORATE SOURCE: Univ. of Missouri, Columbia
SOURCE: Science (Washington, DC, United States) (1954), 120, 455-6
CODEN: SCIEAS; ISSN: 0036-8075
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB Cellulose digestion by rumen microorganisms in vitro was increased by addition of cholesterol (I), stilbestrol (II), or estrone (III) to the fermentation mixture The average percentage digestion of cellulose in basal ration, 35.1-36.7%, was increased to 48.4, 51.4, and 57.3% by 20 γ of I, II, and III, resp. The coefficient of digestibility of cellulose and of **protein** was increased 16 and 18%, resp., by addition of 10 or 20

mg./day of II to the basal ration of crossbred yearling wethers. When II was maintained in the diet beyond the test period (18 days), toxic symptoms (anorexia, listlessness, edema, abdominal pain, and enlargement of the urethra and prostate) were observed. Removal of II from the diet and subcutaneous injection of 100 mg. testosterone produced rapid recoveries.

L17 ANSWER 22 OF 22 HCAPLUS COPYRIGHT 2005 ACS on STN
ACCESSION NUMBER: 1925:13188 HCAPLUS
DOCUMENT NUMBER: 19:13188
ORIGINAL REFERENCE NO.: 19:1734h-i
TITLE: The physiological action of non-specific antigen prepared from shattered hemoproteins
AUTHOR(S): **Brooks, C.**; Pack, G. T.; Goode, H.
SOURCE: Proceedings of the Society for Experimental Biology and Medicine (1924), 21, 321-6
CODEN: PSEBAA; ISSN: 0037-9727
DOCUMENT TYPE: Journal
LANGUAGE: Unavailable
AB Ox blood fibrin was treated with HCl and pepsin. The residue was fractioned by precipitation with (NH4)2SO4 and the lower secondary proteoses were obtained. When these were given intravenously to man in doses of 15-40 mg. every 48 hrs., there was no reaction such as occurs when **protein** is injected. The antigen is desensitizing and acts as a non-specific immunizing substance.

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         (c) 2005 BIOSIS
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         (c) 2005 Inst for Sci Info
File  71:ELSEVIER BIOBASE 1994-2005/Oct W2
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S1         63   FHOS OR FORMIN(W)HOMOLOGUE
S2         22   RD (unique items)
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 2/AB/1     (Item 1 from file: 155)
DIALOG(R)File 155:MEDLINE(R)
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18598649   PMID: 15966898
  Fhos2,  a  novel  formin-related actin-organizing protein, probably
associates with the nestin intermediate filament.
  Kanaya Hideki; Takeya Ryu; Takeuchi Kosei; Watanabe Norinobu; Jing Naihe;
Sumimoto Hideki
  Medical  Institute  of  Bioregulation, Kyushu University, 3-1-1 Maidashi,
Higashi-ku, Fukuoka 812-8582, Japan.
  Genes  to cells - devoted to molecular & cellular mechanisms (England)
Jul 2005,  10  (7)  p665-78,  ISSN 1356-9597   Journal Code: 9607379
  Publishing Model Print
  Document type: Journal Article
  Languages: ENGLISH
  Main Citation Owner: NLM
  Record type: MEDLINE; Completed
  Fhos1 is a mammalian formin-family protein, and functions as an organizer
of the actin microfilament. Here we have cloned human and mouse cDNAs for a
novel Fhos homolog, designated Fhos2.  The messages for Fhos2 are
expressed  in  the  heart, kidney, and brain, where the Fhos1 mRNAs are not
abundant.  Two  splice variants of Fhos2 exist in a tissue-specific manner;
the  longer  variant  Fhos2L  is  the  major form in the heart, whereas the
kidney  and  brain  predominantly  express  Fhos2S  that  encodes a shorter
protein.  Over-expression  of  an active form of the two Fhos2 variants, as
well as that of Fhos1, induces the formation of actin stress fibers in HeLa
cells,  suggesting  that  Fhos2  acts  as  an actin-organizing protein.
Biochemical  analysis  using  rat cardiomyoblastic H9c2 (2-1) cells reveals
that  endogenous  Fhos2  is enriched in the intermediate filament fraction.
Consistent  with  this, Fhos2 localizes to the nestin intermediate filament
but  not  to other cytoskeletons, as demonstrated by staining of H9c2 (2-1)
cells  with  anti-Fhos2  antibodies.  Furthermore,  Fhos2  is  present  in
nestin-expressing neuroepithelial cells of the fetal rat brain. Thus, Fhos2
not only has the actin-organizing activity but also associates with nestin,
which  may  imply  a  Fhos2-mediated  link  between the nestin intermediate
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filament and actin microfilament.

2/AB/2 (Item 2 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

18506947 PMID: 15878344
FHOD1 coordinates actin filament and microtubule alignment to mediate cell elongation.
Gasteier Judith E; Schroeder Sebastian; Muranyi Walter; Madrid Ricardo; Benichou Serge; Fackler Oliver T
Abteilung Virologie, Universitatsklinikum Heidelberg, INF 324, D-69120 Heidelberg, Germany.
Experimental cell research (United States) May 15 2005, 306 (1) p192-202, ISSN 0014-4827 Journal Code: 0373226
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Diaphanous-related formins (DRFs) are actin nucleators that mediate rearrangements of the actin cytoskeleton downstream of specific Rho GTPases. The DRF Formin Homology 2 Domain containing 1 (FHOD1) interacts with the Rac1 GTPase and induces the formation of and associates with bundled actin stress fibers. Here we report that active FHOD1 also coordinates microtubules with these actin stress fibers. Expression of a constitutive active FHOD1 variant in HeLa cells not only resulted in pronounced formation of FHOD1-actin fibers but also caused marked cell elongation and parallel alignment of microtubules without affecting cytokinesis of these cells. The analysis of deletions in the FH1 and FH2 functional regions revealed that the integrity of both domains was strictly required for FHOD1's effects on the cytoskeleton. Dominant-negative approaches demonstrated that filament coordination and cell elongation depended on the activity of the Rho-ROCK cascade, but did not involve Rac or Cdc42 activity. Experimental depolymerization of actin filaments or microtubules revealed that the formation of FHOD1-actin fibers was a prerequisite for the polarization of microtubules. However, only simultaneous disruption of both filament systems reversed the cell elongation induced by activated FHOD1. Thus, sustained cell elongation was a consequence of FHOD1-mediated actin-microtubule coordination. These results suggest filament coordination as a conserved function of mammalian DRFs.

2/AB/3 (Item 3 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

17455978 PMID: 15642356
Oligomerization of the diaphanous-related formin FHOD1 requires a coiled-coil motif critical for its cytoskeletal and transcriptional activities.
Madrid Ricardo; Gasteier Judith E; Bouchet Jerome; Schroder Sebastian; Geyer Matthias; Benichou Serge; Fackler Oliver T
Department of Infectious Diseases, Institut Cochin, INSERM U567, CNRS UMR 8104, Universite Paris V, 27 Rue du Faubourg Saint-Jacques, 75014 Paris, France.
FEBS letters (Netherlands) Jan 17 2005, 579 (2) p441-8, ISSN 0014-5793 Journal Code: 0155157

Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

The diaphanous-related formin homology 2 domain containing protein 1 (FHOD1) interacts with the Rac GTPase and activates the Rho-ROCK cascade leading to the formation of actin stress fibers. Here, we report the detection of homotypic interactions of FHOD1 in the yeast two-hybrid system, by co-immunoprecipitation and co-localization in mammalian cells. A predicted coiled-coil motif C-terminal to the core FH2 domain, but not the core FH2 domain itself, was critical for self-association of FHOD1. Deletion of both the coiled-coil motif and the core FH2 domain abrogated formation of actin stress fibers and activation of transcription of the serum response element by FHOD1. In contrast, these motifs were dispensable for the physical and functional interaction of FHOD1 with Rac1. Together, these results indicate that oligomerization of FHOD1 via the coiled-coil motif is a critical parameter for its biological activities.

2/AB/4 (Item 4 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

17453133 PMID: 15473682
Riboproteomics of the hepatitis C virus internal ribosomal entry site.
Lu Henry; Li Weiqun; Noble William Stafford; Payan Donald; Anderson D C
Rigel, Inc., South San Francisco, California 94066, USA.
Journal of proteome research (United States) Sep-Oct 2004, 3 (5) p949-57, ISSN 1535-3893 Journal Code: 101128775
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

Hepatitis C virus (HCV) protein translation is mediated by a cis-acting RNA, an internal ribosomal entry site (IRES), located in the 5' nontranslated region of the viral RNA. To examine proteins bound to the IRES, which could include proteins important for its function as well as potential drug targets, we used shotgun peptide sequencing to identify proteins in quadruplicate protein affinity extracts of lysed Huh7 cells, obtained using a biotinylated IRES. Twenty-six proteins bound the HCV IRES but not a reversed complementary sequence RNA or vector RNA controls. These included five ribosomal subunits, nine eukaryotic initiation factor 3 subunits, and novel interacting proteins such as the cytoskeletal-related proteins actin, **FHOS** (**formin homologue** overexpressed in spleen) and MIP-T3 (microtubule interacting protein that associates with TRAF3). Other novel HCV IRES-binding proteins included UNR (upstream of N-ras), UNR-interacting protein, and the RNA-binding proteins PAI-1 (plasminogen activator inhibitor-1) mRNA binding protein and Ewing sarcoma breakpoint 1 region protein EWS. A large set of additional proteins bound both the HCV IRES and a reversed complementary IRES sequence control, including the known HCV interactors PTB (polypyrimidine tract binding protein), the La autoantigen, and nucleolin. The discovery of these novel HCV IRES-binding proteins suggests links between IRES biology and the cytoskeleton, signal transduction, and other cellular functions.

2/AB/5 (Item 5 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

16457226 PMID: 15138285
EBV attachment stimulates **FHOS** /FHOD1 redistribution and co-aggregation with CD21: formin interactions with the cytoplasmic domain of human CD21.
Gill Michael B; Roecklein-Canfield Jennifer; Sage David R; Zambela-Soediono Maria; Longtine Nina; Uknis Marc; Fingeroth Joyce D
Division of Infectious Diseases, Beth Israel Deaconess Medical Center, Boston, MA 02115, USA.
Journal of cell science (England) Jun 1 2004, 117 (Pt 13) p2709-20, ISSN 0021-9533 Journal Code: 0052457
Contract/Grant No.: R01 DE 12186; DE; NIDCR
Publishing Model Print-Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
CD21 is a multifunctional receptor for Epstein-Barr virus (EBV), for C3dg and for CD23. Upon engagement of immune complexes CD21 modulates immunoreceptor signaling, linking innate and adaptive immune responses. The mechanisms enabling CD21 to independently relay information between the exterior and interior of the cell, however, remain unresolved. We show that **formin homologue** overexpressed in spleen (**FHOS**/FHOD1) binds the cytoplasmic domain of human CD21 through its C terminus. When expressed in cells, EGFP-**FHOS** localizes to the cytoplasm and accumulates with actin in membrane protrusions. Plasma membrane aggregation, redistribution and co-localization of both proteins are stimulated when EBV (ligand) binds CD21. Though widely expressed, **FHOS** RNA is most abundant in the littoral cell, a major constituent of the red pulp of human spleen believed to function in antigen filtration. Formins are molecular scaffolds that nucleate actin by a pathway distinct from Arp2/3 complex, linking signal transduction to actin reorganization and gene transcription. Thus, ligand stimulation of **FHOS** -CD21 interaction may transmit signals through promotion of cytoskeletal rearrangement. Moreover, formin recruitment to sites of actin assembly initiated by immunoreceptors could be a general mechanism whereby co-receptors such as CD21 modulate intracellular signaling.

2/AB/6 (Item 6 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

16323781 PMID: 15095401
Identification of FHOD1-binding proteins and mechanisms of FHOD1-regulated actin dynamics.
Westendorf Jennifer J; Koka Sreenivas
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Journal of cellular biochemistry (United States) May 1 2004, 92 (1) p29-41, ISSN 0730-2312 Journal Code: 8205768
Contract/Grant No.: 1P20RR081759-010004; RR; NCRR
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Formin homology-2-domain containing protein 1 (FHOD1) regulates gene transcription, actin-cytoskeleton structure, and cell migration. To gain

insight into the mechanisms by which FHOD1 mediates these diverse activities, a yeast-two-hybrid screen was performed to identify FHOD1-binding proteins. Three proteins specifically interacted with the carboxy-terminal two-thirds of FHOD1, which includes the FH1, FH2, and diaphanous activating domains (DAD). The newly identified FHOD1-binding proteins are protein kinase C binding protein 1 (PRKCBP1), cyclophilin B, and an isoform of WASP-interacting SH3-domain protein/diaphanous-interactin g protein 1 (WISH/DIP1), named WISH-B. The proline-rich FH1 domain of FHOD1 was sufficient to interact with the central portion of PRKCP1 and full-length cyclophilin B. The FH1 domain also interacted with full-length WISH-B, but the extreme amino-terminus was sufficient to associate with WISH-B as well. WISH-B altered the solubility of FHOD1 in vitro and a truncation mutant containing the amino-terminal 227 residues of WISH-B disrupted FHOD1-induced stress fibers. WISH-B did not affect FHOD1-induced gene transcription through the serum response factor (SRF) recognition site on the skeletal alpha actin promoter (SkA). However, stabilization of F-actin prevented FHOD1 dependent activation of this promoter in presence of high, but not low serum concentrations. Thus, the identification of a new FHOD1-binding protein provides insight into the mechanisms by which FHOD1 regulates actin polymerization and transcription. Copyright 2004 Wiley-Liss, Inc.

2/AB/7 (Item 7 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15360565 PMID: 15051728

Formin homology domain protein (FHOD1) is a cyclic GMP-dependent protein kinase I-binding protein and substrate in vascular smooth muscle cells.

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Journal of biological chemistry (United States) Jun 4 2004, 279 (23) p24420-6, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: R01 HL55309; HL; NHLBI

Publishing Model Print-Electronic

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Cyclic GMP-dependent protein kinase I (PKGI) mediates vascular relaxation by nitric oxide and related nitrovasodilators and inhibits vascular smooth muscle cell (VSMC) migration. To identify VSMC proteins that interact with PKGI, the N-terminal protein interaction domain of PKGIalpha was used to screen a yeast two-hybrid human aortic cDNA library. The formin homology (FH) domain-containing protein, FHOD1, was found to interact with PKGIalpha in this screen. FH domain-containing proteins bind Rho-family GTPases and regulate actin cytoskeletal dynamics, cell migration, and gene expression. Antisera to FHOD1 were raised and used to characterize FHOD1 expression and distribution in vascular cells. FHOD1 is highly expressed in human coronary artery, aortic smooth muscle cells, and in human arterial and venous endothelial cells. In glutathione S-transferase pull-down experiments, the FHOD1 C terminus (amino acids 964-1165) binds full-length PKGI. Both in vitro and intact cell studies demonstrate that the interaction between FHOD1 and PKGI is decreased 3- to 5-fold in the presence of the PKG activator, 8Br-cGMP. Immunofluorescence studies of human VSMC show that FHOD1 is cytoplasmic and is concentrated in the perinuclear region. PKGI also directly phosphorylates FHOD1, and studies with wild-type and mutant

FHOD1-derived peptides identify Ser-1131 in the FHOD1 C terminus as the unique PKGI phosphorylation site in FHOD1. These studies demonstrate that FHOD1 is a PKGI-interacting protein and substrate in VSMCs and show that cyclic GMP negatively regulates the FHOD1-PKGI interaction. Based on the known functions of FHOD1, the data are consistent with a role for FHOD1 in cyclic GMP-dependent inhibition of VSMC stress fiber formation and/or migration.

2/AB/8 (Item 8 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15291536 PMID: 15067022
Pheromone-induced polarization is dependent on the Fus3p MAPK acting through the formin Bni1p.
Matheos Dina; Metodiev Metodi; Muller Eric; Stone David; Rose Mark D
Department of Molecular Biology, Princeton University, Princeton, NJ 08544-1014, USA.
Journal of cell biology (United States) Apr 2004, 165 (1) p99-109, ISSN 0021-9525 Journal Code: 0375356
Contract/Grant No.: GM37739; GM; NIGMS
Publishing Model Print-Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
During mating, budding yeast cells reorient growth toward the highest concentration of pheromone. Bni1p, a **formin homologue**, is required for this polarized growth by facilitating cortical actin cable assembly. Fus3p, a pheromone-activated MAP kinase, is required for pheromone signaling and cell fusion. We show that Fus3p phosphorylates Bni1p in vitro, and phosphorylation of Bni1p in vivo during the pheromone response is dependent on Fus3p. fus3 mutants exhibited multiple phenotypes similar to bni1 mutants, including defects in actin and cell polarization, as well as Kar9p and cytoplasmic microtubule localization. Disruption of the interaction between Fus3p and the receptor-associated Galpha subunit caused similar mutant phenotypes. After pheromone treatment, Bni1p-GFP and Spa2p failed to localize to the cortex of fus3 mutants, and cell wall growth became completely unpolarized. Bni1p overexpression suppressed the actin assembly, cell polarization, and cell fusion defects. These data suggest a model wherein activated Fus3p is recruited back to the cortex, where it activates Bni1p to promote polarization and cell fusion.

2/AB/9 (Item 9 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15237179 PMID: 15010865
Identification and characterization of human FHOD3 gene in silico.
Katoh Masuko; Katoh Masaru
M&M Medical BioInformatics, Narashino 275-0022, Japan. mkatoh@ncc.go.jp
International journal of molecular medicine (Greece) Apr 2004, 13 (4) p615-20, ISSN 1107-3756 Journal Code: 9810955
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

Formin homology proteins are actin regulators with scaffold function, which are implicated in organogenesis, normal tissue homeostasis, and cancer-cell invasion. FHOD1/**FHOS** , GRID2IP, Fmn1 and Fmn2 are non-FDD-type Formin homology proteins, while FMNL1, FMNL2/FHOD2, FMNL3, DAAM1, DAAM2, DIAPH1, DIAPH2 and DIAPH3 are FDD-type Formin homology proteins. Here, we identified and characterized FHOD3 (also known as FHOS2), a novel gene homologous to FHOD1, by using bioinformatics. Because FLJ46173, FLJ22297, KIAA1695 and FLJ34580 were partial FHOD3 cDNAs, complete coding sequence of FHOD3 cDNA was determined by assembling nucleotide sequences of FLJ46173 and FLJ22297. FHOD3 gene at human chromosome 18q12.2 was found consisting of at least 25 exons. Exon 11 of FHOD3 gene was spliced out in KIAA1695 cDNA and BF116064 EST, while exon 13 of FHOD3 gene was spliced out in FLJ46173 cDNA. FHOD3 gene encodes at least three isoforms due to alternative splicing of the exon skipping type. FHOD3 and FHOD1 showed 52.1% total-amino-acid identity. Drosophila CG32030 showed 43.9% total-amino-acid identity with human FHOD3, and 39.1% total-amino-acid identity with human FHOD1. FHDHN domain (codon 1-327 of FHOD3) and FHDHC domain (codon 1377-1421 of FHOD3) were identified as the N-terminal conserved region and the juxta C-terminal conserved region, respectively. Human FHOD3, FHOD1 and Drosophila CG32030 were found to share the conserved domain structure consisting of FHDHN, FH1, FH2, and FHDHC domains. This is the first report on the FHOD3 gene as well as on the novel FHDHN and FHDHC domains.

2/AB/10 (Item 10 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

15030359 PMID: 14576350

Fhos , a mammalian formin, directly binds to F-actin via a region N-terminal to the FH1 domain and forms a homotypic complex via the FH2 domain to promote actin fiber formation.

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Publishing Model Print

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

Formins constitute a family of eukaryotic proteins that are considered to function as a cytoskeleton organizer to regulate morphogenesis, cell polarity and cytokinesis. **Fhos** is a recently identified mammalian formin, which contains the conserved domains FH (formin homology) 1 and FH2 in the middle region and the Dia-autoregulatory domain (DAD) in the C-terminus. The role of **Fhos** in the regulation of cytoskeleton, however, has remained unknown. Here we show that **Fhos**, in an active form, induces the formation of actin stress fibers and localizes to the actin-based structure. **Fhos** appears to normally exist in a closed inactive form via an intramolecular interaction between the N-terminal region and the C-terminal DAD. Both FH1 and FH2 domains are required for the induction of the stress fiber formation. However, the N-terminal region of **Fhos** is required for the targeting of this protein to stress fibers, which is probably mediated via its F-actin-binding activity. We also show that **Fhos** occurs as a homotypic complex in cells. The self-association of **Fhos** seems to be mediated via the FH2 domain: the domains bind to each other in a direct manner. Thus, the mammalian formin

Fhos , which directly binds to F-actin via the N-terminal region, forms a homotypic complex via the FH2 domain to organize actin cytoskeleton.

2/AB/11 (Item 11 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

14990580 PMID: 12857739
Activation of the Rac-binding partner FHOD1 induces actin stress fibers via a ROCK-dependent mechanism.
Gasteier Judith E; Madrid Ricardo; Krautkramer Ellen; Schroder Sebastian; Muranyi Walter; Benichou Serge; Fackler Oliver T
Institute for Hygiene, Department of Virology, University of Heidelberg, 69120 Heidelberg, Germany.
Journal of biological chemistry (United States) Oct 3 2003, 278 (40) p38902-12, ISSN 0021-9258 Journal Code: 2985121R
Publishing Model Print-Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
Diaphanous related formins (DRFs) are part of the formin protein family that control morphogenesis, embryonic differentiation, cytokinesis, and cell polarity. DRFs organize the cytoskeleton in eukaryotic cells via the interaction with specific members of the Rho family of small GTPases including Rho, Rac, and Cdc42. This is best understood for Rho, which transmits signals to the actin cytoskeleton through the cooperation of its DRF effector mDia with ROCK (Rho-associated kinase). Here, we show that a constitutive active form of the Rac-interacting DRF FHOD1 (formin homology 2 domain containing 1) associates with F-actin in NIH3T3 cells, resulting in the formation of thick actin fibers. Cytoskeletal changes induced by FHOD1 correlated with the induction of serum response element transcription and were mediated by formin homology domains 1 and 2 of FHOD1. FHOD1-induced effects required the activity of the Rho-ROCK cascade that is targeted at a level downstream of Rho by the DRF. However, when the functional interaction of FHOD1 with individual GTPases was addressed, Rac but not Rho or Cdc42 bound to FHOD1 in cells and induced its recruitment to actin filaments and lamellipodia/membrane ruffles. Furthermore, activated FHOD1 interfered with lamellipodia formation. These results indicate that FHOD1 acts as an effector of Rac in actin rearrangements and transcriptional regulation and may provide a link for the Rac-dependent activation of the Rho cascade.

2/AB/12 (Item 12 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

14855569 PMID: 12677009
The Formin family protein, formin homolog overexpressed in spleen, interacts with the insulin-responsive aminopeptidase and profilin IIa.
Tojo Hideaki; Kaieda Isao; Hattori Harumi; Katayama Nozomi; Yoshimura Koji; Kakimoto Shigeya; Fujisawa Yukio; Presman Eleonora; Brooks Cydney C; Pilch Paul F
Discovery Research Laboratories II, Pharmaceutical Research Division, Takeda Chemical Industries Co., Ltd., Tsukuba, Ibaraki 300-4293, Japan. Tojo Hideaki@takeda.co.jp
Molecular endocrinology (Baltimore, Md.) (United States) Jul 2003, 17

(7) p1216-29, ISSN 0888-8809 Journal Code: 8801431
Contract/Grant No.: DK-30425; DK; NIDDK
Publishing Model Print-Electronic
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

Insulin stimulates translocation of glucose transporter isoform type 4 (GLUT4) and the insulin-responsive aminopeptidase (IRAP) from an intracellular storage pool to the plasma membrane in muscle and fat cells. A role for the cytoskeleton in insulin action has been postulated, and the insulin signaling pathway has been well investigated; however, the molecular mechanism by which GLUT4/IRAP-containing vesicles move from an interior location to the cell surface in response to insulin is incompletely understood. Here, we have screened for IRAP-binding proteins using a yeast two-hybrid system and have found that the C-terminal domain of **FHOS** (formin homolog overexpressed in spleen) interacts with the N-terminal cytoplasmic domain of IRAP. **FHOS** is a member of the Formin/Diaphanous family of proteins that is expressed most abundantly in skeletal muscle. In addition, there are two novel types of **FHOS** transcripts generated by alternative mRNA splicing. FHOS78 has a 78-bp insertion and it is expressed mainly in skeletal muscle where it may be the most abundant isoform in humans. The ubiquitously expressed FHOS24 has a 24-bp insertion encoding an in-frame stop codon that results in a truncated polypeptide. It is known that some formin family proteins interact with the actin-binding profilin proteins. Both **FHOS** and FHOS78 bound to profilin IIa via their formin homology 1 domains, but neither bound profilin I or IIb. Overexpression of **FHOS** and FHOS78 resulted in enhanced insulin-stimulated glucose uptake in L6 cells to similar levels. However, overexpression of FHOS24, lacking the IRAP-binding domain, did not affect insulin-stimulated glucose uptake. These findings suggest that **FHOS** mediates an interaction between GLUT4/IRAP-containing vesicles and the cytoskeleton and may participate in exocytosis and/or retention of this membrane compartment.

2/AB/13 (Item 13 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

14719246 PMID: 12665555
The formin-homology-domain-containing protein FHOD1 enhances cell migration.
Koka Sreenivas; Neudauer Cheryl L; Li Xiaodong; Lewis Robert E; McCarthy James B; Westendorf Jennifer J
Department of Oral Biology, College of Dentistry, University of Nebraska Medical Center, Lincoln, NE 68583, USA.
Journal of cell science (England) May 1 2003, 116 (Pt 9) p1745-55, ISSN 0021-9533 Journal Code: 0052457
Contract/Grant No.: P30 CA 77598; CA; NCI; R01 CA 82295; CA; NCI
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed

Formin-homology-domain-containing proteins interact with Rho-family GTPases and regulate actin cytoskeleton organization and gene transcription. FHOD1 is a member of this family, interacts with Rac1 and induces transcription from the serum response element. In this study, we examined the effects of FHOD1 expression on cytoskeletal organization and

function in mammalian cells. FHOD1 proteins were stably expressed in WM35 melanoma cells and NIH-3T3 fibroblasts. Cells expressing full-length FHOD1 demonstrated an elongated phenotype compared with vector-transfected cells and cells expressing a truncated FHOD1 (1-421) that lacks the conserved FH1 and FH2 domains. Full-length FHOD1 co-localized with filamentous actin at cell peripheries. Cells transiently expressing a C-terminal FHOD1 truncation mutant (DeltaC, residues 1-1010), which lacks an autoinhibitory protein-protein interaction domain, displayed prominent stress fibers. FHOD1 (1-421) did not induce stress fibers but localized to membrane ruffles in a manner similar to the full-length protein, indicating that the FH1 and FH2 domains are required for stress fiber appearance. FHOD1 DeltaC (1-1010)-dependent stress fibers were sensitive to dominant-negative RacN17 and the RhoA and ROCK inhibitors, C3 transferase and Y-27632. Stable overexpression of full-length FHOD1 enhanced the migration of WM35 and NIH-3T3 cells to type-I collagen and fibronectin, respectively. Cells expressing FHOD1 (1-421) migrated similar to control cells. Integrin expression and activation were not affected by FHOD1 expression. Moreover, FHOD1 overexpression did not alter integrin usage during adhesion or migration. These data demonstrate that FHOD1 interacts with and regulates the structure of the cytoskeleton and stimulates cell migration in an integrin-independent manner.

2/AB/14 (Item 14 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

13973716 PMID: 11590143

The formin/diaphanous-related protein, **FHOS**, interacts with Rac1 and activates transcription from the serum response element.

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Journal of biological chemistry (United States) Dec 7 2001, 276 (49) p46453-9, ISSN 0021-9258 Journal Code: 2985121R

Contract/Grant No.: F32-CA77167; CA; NCI

Publishing Model Print-Electronic

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: MEDLINE; Completed

FHOS is a member of the formin homology (FH) family of proteins and is expressed at high levels in splenic cells. FH proteins link cellular signaling pathways to the actin cytoskeleton and serum response factor-dependent transcription. In these studies, the role of **FHOS** in Rho family GTPase signaling pathways was analyzed. **FHOS** interacted with the polybasic domain in the Rac1 C terminus in a guanine nucleotide-independent manner but did not interact with RhoA, Cdc42Hs, Rac2, or Rac3. Intramolecular autoinhibitory interactions between the C terminus of **FHOS** and an N-terminal region partially overlapping the Rac1 interaction domain were also identified. **FHOS** truncation mutants lacking the N- or C-terminal autoregulatory domains stimulated transcription of a c-fos serum response element (SRE)-driven reporter. Overexpression of wild-type and mutant (N17 and V12) Rac1 proteins repressed SRE induction by the N-terminal **FHOS** deletion mutant but not by the C-terminal **FHOS** deletion mutant. Immunofluorescence studies indicated that the localization of the mutant **FHOS** proteins might contribute to their differential responses to Rac1. Wild-type **FHOS** and the N-terminal deletion mutant localized to the perinuclear

region and membrane edges. In contrast, the C-terminal **FHOS** mutants were diffusely localized. These data suggest that **FHOS** induces transcription from SREs by multiple pathways and that Rac1 may influence the course of some **FHOS**-induced signaling events.

2/AB/15 (Item 15 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

13393821 PMID: 10352228
Identification and characterization of a protein containing formin homology (FH1/FH2) domains.
Westendorf J J; Mernaugh R; Hiebert S W
Vanderbilt University, Department of Biochemistry and Vanderbilt Cancer Center, Nashville, TN 37232, USA.
Gene (NETHERLANDS) May 31 1999, 232 (2) p173-82, ISSN 0378-1119 Journal Code: 7706761
Contract/Grant No.: RO1-AG13726; AG; NIA; RO1-CA64140; CA; NCI; RO1-CA77274; CA; NCI; +
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
A novel member of the Formin/Diaphanous family of proteins was cloned and characterized. A 4kB mRNA is ubiquitously expressed but is found in abundance in the spleen. **FHOS** (**Formin Homologue** Overexpressed in Spleen) contains a 3414bp open reading frame and encodes for an approximately 128kDa protein. **FHOS** has sequence homology to Diaphanous and Formin proteins within the Formin Homology (FH)1 and FH2 domains. **FHOS** also contains a coiled-coil, a collagen-like domain, two nuclear localization signals, and several potential PKC and PKA phosphorylation sites. **FHOS**-specific antiserum was generated and used to determine that **FHOS** is a predominantly cytoplasmic protein and is expressed in a variety of human cell lines. **FHOS** was mapped to chromosome 16q22 between framework markers WI-5594 and WI-9392.

2/AB/16 (Item 16 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12749469 PMID: 10678165
Diaphanous-related formins bridge Rho GTPase and Src tyrosine kinase signaling.
Tominaga T; Sahai E; Chardin P; McCormick F; Courtneidge S A; Alberts A S
University of California, San Francisco Cancer Center 94115, USA.
Molecular cell (UNITED STATES) Jan 2000, 5 (1) p13-25, ISSN 1097-2765 Journal Code: 9802571
Publishing Model Print
Document type: Journal Article
Languages: ENGLISH
Main Citation Owner: NLM
Record type: MEDLINE; Completed
We have examined the role of the mouse Diaphanous-related formin (DRF) Rho GTPase binding proteins, mDia1 and mDia2, in cell regulation. The DRFs are required for cytokinesis, stress fiber formation, and transcriptional activation of the serum response factor (SRF). 'Activated' mDia1 and mDia2 variants, lacking their GTPase binding domains, cooperated with Rho-kinase

or ROCK to form stress fibers but independently activated SRF. Src tyrosine kinase associated and co-localized with the DRFs in endosomes and in mid-bodies of dividing cells. Inhibition of Src also blocked cytokinesis, SRF induction by activated DRFs, and cooperative stress fiber formation with active ROCK. Our results show that the DRF proteins couple Rho and Src during signaling and the regulation of actin dynamics.

2/AB/17 (Item 17 from file: 155)
DIALOG(R)File 155:MEDLINE(R)

12640197 PMID: 10556060
Mutations in the Rho1 small GTPase disrupt morphogenesis and segmentation during early Drosophila development.
Magie C R; Meyer M R; Gorsuch M S; Parkhurst S M
Division of Basic Sciences and Program in Developmental Biology, A1-162, Fred Hutchinson Cancer Research Center, Seattle, WA 98109, USA.
Development (Cambridge, England) (ENGLAND) Dec 1999, 126 (23) p5353-64, ISSN 0950-1991 Journal Code: 8701744
Contract/Grant No.: GM47852; GM; NIGMS
Publishing Model Print
Document type: Journal Article
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Main Citation Owner: NLM
Record type: MEDLINE; Completed
Rho GTPases play an important role in diverse biological processes such as actin cytoskeleton organization, gene transcription, cell cycle progression and adhesion. They are required during early Drosophila development for proper execution of morphogenetic movements of individual cells and groups of cells important for the formation of the embryonic body plan. We isolated loss-of-function mutations in the Drosophila Rho1 (Rho1) gene during a genetic screen for maternal-effect mutations, allowing us to investigate the specific roles Rho1 plays in the context of the developing organism. Here we report that Rho1 is required for many early events: loss of Rho1 function results in both maternal and embryonic phenotypes. Embryos homozygous for the Rho1 mutation exhibit a characteristic zygotic phenotype, which includes severe defects in head involution and imperfect dorsal closure. Two phenotypes are associated with reduction of maternal Rho1 activity: the actin cytoskeleton is disrupted in egg chambers, especially in the ring canals and embryos display patterning defects as a result of improper maintenance of segmentation gene expression. Despite showing imperfect dorsal closure, Rho1 does not activate downstream genes or interact genetically with members of the JNK signaling pathway, used by its relatives dRac and dCdc42 for proper dorsal closure. Consistent with its roles in regulating actin cytoskeletal organization, we find that Rho1 interacts genetically and physically with the Drosophila **formin homologue** , cappuccino. We also show that Rho1 interacts both genetically and physically with concertina, a G(alpha) protein involved in cell shape changes during gastrulation.

2/AB/18 (Item 1 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0014918803 BIOSIS NO.: 200400289560
Reduction of Fe(III) (Hydr)oxides with known thermodynamic stability by Geobacter metallireducens
AUTHOR: Dominik Peter (Reprint); Kaupenjohann Martin

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JOURNAL: Geomicrobiology Journal 21 (4): p287-295 June 2004 2004
MEDIUM: print
ISSN: 0149-0451
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Sulfate-reducing and methanogenic microorganisms become inactive when the concentration of the electron donors drops below a threshold set by the minimum Gibbs free energy required for the bacterial metabolism to be maintained. Thus, their activity is thermodynamically controlled. In this paper we study if the activity of dissimilatory Fe(III) reducing bacteria is also limited by the thermodynamics of the reaction. We synthesized five Fe(III) (hydr)oxides (**FHOs**) of moderate stability and determined the solubility product (log KSO (-39.1)-(-41.8)), in order to calculate their standard free energy of formation. KSO values, estimated from the particle size did not correspond with experimentally determined ones. HCO3- and PIPES-buffered media, containing 45 mM FHO and either 1, 10, or 100 mM acetate were inoculated with Geobacter metallireducens . At the end of bacterial reduction, the Gibbs free energy of the reaction showed significant differences between the different **FHOs**. The termination of the bacterial activity was consequently not triggered thermodynamically. However, the non-dissolved Fe(II) (HCl-soluble minus soluble Fe(II)) showed an excellent correlation with the surface of the **FHOs** (15 mumol m-2). It is therefore likely that the termination of the reaction was caused by blocking of the FHO surface with insoluble Fe(II), as has been previously reported in the literature. The ecological significance of both thermodynamic limitation and surface availability limitation is discussed for **FHOs** of different K SO in environments with approximately neutral pH.

2/AB/19 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0012929877 BIOSIS NO.: 200100101716
Identification and cloning of AtFORMIN1, an Arabidopsis thaliana **formin homologue**
AUTHOR: Cvrckova F (Reprint); Bavlnka B (Reprint); Zarsky V
AUTHOR ADDRESS: Dept. of Plant Physiology, Faculty of Sciences, Charles University, Vinicna 5, CZ 128 44, Praha, 2, Czech Republic**Czech Republic
JOURNAL: Biochemical Society Transactions 28 (5): pA208 October, 2000 2000
MEDIUM: print
CONFERENCE/MEETING: 18th International Congress of Biochemistry and Molecular Biology Birmingham, UK July 16-20, 2000; 20000716
SPONSOR: International Union of Biochemistry and Molecular Biology
Federation of European Biochemical Societies
Biochemical Society
ISSN: 0300-5127
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Citation
LANGUAGE: English

2/AB/20 (Item 1 from file: 357)

DIALOG(R)File 357:Derwent Biotech Res.

0370752 DBR Accession No.: 2005-16458 PATENT
Novel isolated protein comprising **FHOS** or its homolog, derivative or fragment, interacting with proteins chosen from group of GROUP1 e.g. mRNF23, mERp59 or mBRD7(627), useful for screening its modulator - **FHOS** protein gene transfer and expression in host cell for modulator drug screening and disease therapy
AUTHOR: SAKAMOTO T; TAKEDA S
PATENT ASSIGNEE: SAKAMOTO T; TAKEDA S 2005
PATENT NUMBER: US 20050100966 PATENT DATE: 20050512 WPI ACCESSION NO.: 2005-345401 (200535)
PRIORITY APPLIC. NO.: US 805684 APPLIC. DATE: 20040319
NATIONAL APPLIC. NO.: US 805684 APPLIC. DATE: 20040319
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - An isolated protein (I) comprising a first protein, which is **FHOS** or its homolog, derivative or fragment, interacting with a second protein chosen from a group of GROUP1 e.g. mRNF23, mERp59 or mBRD7(627), where the interaction is through a complex or covalent bond, or any other intermolecular interaction, is new. DETAILED DESCRIPTION - An isolated protein (I) comprising a first protein which is **FHOS** or its homolog, derivative or fragment, interacting with a second protein chosen from group a of GROUP1 e.g. mRNF23, mERp59, mBRD7(627), mSPNA1, mVCP, mSTAT5A, mTAKEDA009, mPTRF, mAK031693, m1200014P03Rik, mNNP1, mLOC213473(195), mGOLGA3, mMYG1-pending, mAK044679(668), RS21C6, KIAA0562, COPB, MYH7, KIAA1633, KIAA1288(1191), mVCL, mBC028274(908), mBC026864(777), m5730504C04Rik, mMYH9, mp116Rip, TPM3, MYH6, mMBLR, mZFP144, ZNF144(294), 14-3-3epsilon, BF672897(87), mCATNB, mCATNS, mSWAN, m2300003P22Rik(248), mTAKEDA015, PCNT2, KPNA4, MAPKAP1, mTPT1, mAK014397(679), mHRMT1L1, HRMT1L1(241), SAT(204), BC023995(305), TTN, mLRRFIP1, mAPC2, mCYLN2(1047), mACTN3, mDTNBP1, mTAKEDA013, m14-3-3g, m14-3-3zeta, 14-3-3zeta, m14-3-3b, m14-3-3theta, 14-3-3theta, mSPNB2, BC020494(124), MACF1, MYH1, mPPGB, mZYX, mPRKCABP and mMYLK or its homologue, derivative or fragment, where the interaction is through a complex or covalent bond, or any other intermolecular interaction. INDEPENDENT CLAIMS are also included for the following: (1) producing (I), involves providing a first protein and a second protein under conditions such that the first and second proteins contact each other; (2) detecting (I) in a sample, involves contacting the sample with an antibody chosen from an antibody specific (I); (3) determining whether a compound is capable of modulating an interaction between a first polypeptide (**FHOS**) or its homolog, derivative of fragments) and a second polypeptide as mentioned in (I), involves expressing in an isolated host cell in the presence of a test compound, a first hybrid protein having a DNA binding domain fused to the first polypeptide, a second hybrid protein having a transcription-activating domain fused to the second polypeptide and a reporter gene, where the expression of the reporter gene is dependent on the interaction between the first polypeptide and the second polypeptide, and detecting the expression of the reporter gene; and (4) modulating (M1) the function or activity of (I) in cells of a specific tissue of a mammal, involves delivering to the specific tissue, a selected compound for modulating the function or activity of (I); and. The original spec only gives claims from 192 onwards. BIOTECHNOLOGY - Preferred Protein: In (I), the first and second protein consists of a fully defined 10 or 76 amino acid sequence, available in electronic form from the ISPTO web site http://seqdata.uspto.gov/sequence.html;Document ID:=20050100966, respec tively. The first protein is a hybrid protein containing the complete

amino acid sequence of **FHOS** . ACTIVITY - Antiinflammatory; Neuroprotective; Cytostatic; Cardiovascular-Gen.; Antidiabetic. MECHANISM OF ACTION - Modulator of interaction of **FHOS** and GROUP1. No supporting data is given. USE - (I) is useful for selecting its modulators which involves providing (I), contacting (I) with a test compound and determining binding of the test compound with (I). (M1) is useful for modulating the function or activity of (I) in cells of a specific tissue (claimed), which in turn is useful for treating inflammatory diseases, neurodegenerative diseases, cancer, cardiovascular diseases or diabetes mellitus.ADMINISTRATION - The compound of (M1) is administered by topical or subcutaneous route. No specific dosage detail is given. EXAMPLE - No relevant example is given.(163 pages)

2/AB/21 (Item 2 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0356965 DBR Accession Number: 2005-02669 PATENT
Increasing expression of **formin homologue** overexpressed in spleen (**FHOS**) in a subject, useful for treating diabetes or insulin resistance by administering to a subject a **FHOS** activator, where **FHOS** expression is increased - virus vector-mediated spleen formin homolog gene transfer and expression in host cell for type-II diabetes mellitus or insulin resistance gene therapy
AUTHOR: BROOKS C C
PATENT ASSIGNEE: ADIPOGENIX INC 2004
PATENT NUMBER: US 20040248836 PATENT DATE: 20041209 WPI ACCESSION NO.: 2005-020585 (200502)
PRIORITY APPLIC. NO.: US 627310 APPLIC. DATE: 20030725
NATIONAL APPLIC. NO.: US 627310 APPLIC. DATE: 20030725
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - Increasing expression of **formin homologue** overexpressed in spleen (**FHOS**) in a subject comprises administering to a subject a **FHOS** activator, such that **FHOS** expression is increased. DETAILED DESCRIPTION - INDEPENDENT CLAIMS are also included for: (1) treating diabetes or insulin resistance in a subject by administering to the subject a **FHOS** activator, or the compound identified; (2) identifying compounds for treating diabetes or insulin resistance in a subject by contacting a cell capable of expressing **FHOS** mRNA or protein with a test compound; and determining the effect of the test compound on expression of **FHOS** mRNA or protein, or biological activity of the **FHOS** protein or its portion, where a stimulatory effect is indicative of the compound for treating diabetes or insulin resistance; (3) a compound identified by the method; (4) increasing **FHOS** expression or activity in a cell by contacting the cell with the compound; (5) a pharmaceutical composition comprising a cell that overexpresses **FHOS** protein and a carrier; (6) treating a subject having diabetes or an insulin-resistant subject comprising obtaining cells from the subject, treating the cells with an **FHOS** activator, and administering the treated cells to the subject such that diabetes or insulin-resistance in the subject is treated. BIOTECHNOLOGY - Preferred Method: In increasing expression of **FHOS** in a subject, the **FHOS** protein or mRNA levels are increased. In the methods cited above, the **FHOS** activator is selected from a **FHOS** nucleic acid molecule, a plasmid comprising the **FHOS** nucleic acid molecule, a **FHOS** adenovirus, and a **FHOS** retrovirus. The

activator is also selected from **FHOS** protein, antibody or its biologically active portion, a peptide, peptidimetic, a non-peptide oligomer or a small molecule. In the treatment methods, the subject is suffering from type II diabetes. The cell is a muscle cell, adipocyte or its precursor. Preferred Compound: The compound is formulated with a carrier. ACTIVITY - Antidiabetic. No biological data given. MECHANISM OF ACTION - Gene therapy. USE - The method and compounds are useful for treating diabetes, preferably type II diabetes, or insulin resistance (claimed). ADMINISTRATION - Administration is parenteral, e.g. intravenous, intradermal, subcutaneous, oral (e.g. inhalation), transdermal (topical), transmucosal or rectal. No dosage is given. EXAMPLE - No relevant example given. (24 pages)

2/AB/22 (Item 3 from file: 357)
DIALOG(R)File 357:Derwent Biotech Res.

0296985 DBR Accession Number: 2002-18832 PATENT
Purified complex for treating disorders involving alter levels of the complex, comprises two polypeptides such as insulin-signaling, vesicular-trafficking, calcium-binding or glycogen-binding polypeptides - vector-mediated gene transfer, expression in host cell and antisense oligonucleotide for recombinant protein production, drug screening and gene therapy
AUTHOR: EISEN A J; GIOT L; LEWIN D A
PATENT ASSIGNEE: CURAGEN CORP 2002
PATENT NUMBER: WO 200236766 PATENT DATE: 20020510 WPI ACCESSION NO.: 2002-519252 (200255)
PRIORITY APPLIC. NO.: US 244236 APPLIC. DATE: 20001030
NATIONAL APPLIC. NO.: WO 2001US48162 APPLIC. DATE: 20011030
LANGUAGE: English
ABSTRACT: DERWENT ABSTRACT: NOVELTY - A purified complex (I) comprising 2 polypeptides (P1, P2), where P1 has a sequence of a polypeptide, given in the specification such as PPP1CC, and P2 has a sequence of the corresponding polypeptide given in the specification such as PPP1CC-NOV1, or P1 and P2 comprise the sequence of a first polypeptide-second polypeptide complex (C) selected from 33 complexes such as NAPA1-IP2, is new. DETAILED DESCRIPTION - A new purified complex (I) comprises 2 polypeptides (P1, P2), where P1 has a sequence of a polypeptide, given in the specification such as PPP1CC, and P2 has a sequence of the corresponding polypeptide given in the specification such as PPP1CC-NOV1, or P1 and P2 comprise the sequence of a first polypeptide-second polypeptide complex (C) selected from 33 complexes such as NAPA1-IP2, NAPA1-SYN16, NAPA1-SNAP29, NAPA1-SYN4, NAPA1-LZIP, NAPA1-SNAP25A, PPP1CC-NOV1, PPP1CC-NOV2, PPP1CC-NOV3, PPP1CC-NOV4, PPP1CC-NOV5, PPP1CC-PPP1R5, PPP1CC-KIAA0305, PPP1CC-STAU, PPP1CC-53BP2, PPP1CC-PPP1R10, S100A1-NOV6, S100A1-NOV7, S100A1-NOV8, S100A1-fibrinogen, S100A1-RanBPM, S100A1-profilin II-SV, S100B-NOV9, S100B-NOV10, S100B-NOV11, S100B-fibrinogen, S100B-KIAA0629, S100B-ATP6N1, S100B-synphilin I, S100B-NQO2, S100B-**FHOS**, S100B-S100A9, and S100B-S100A6. INDEPENDENT CLAIMS are also included for the following: (1) a chimeric polypeptide (II) comprising 6 or more amino acids of the first polypeptide of (I) covalently linked to 6 or more amino acids of the second polypeptide of (I); (2) a nucleic acid (III) encoding (II); (3) a pharmaceutical composition (IV) comprising (I); (4) a kit (V) comprising in one or more containers a reagent which can specifically detect (I); (5) detecting (M1) a polypeptide in a biological sample, by: (a) providing a biological sample comprising P1, contacting the biological sample with P2 under conditions suitable for formation of a

complex comprising P1 and P2, and detecting the presence of the complex of P1 and P2, where the presence of the complex indicates the presence of P1 in the sample; or (b) providing a biological sample comprising P2, contacting the biological sample with P1 under conditions suitable for formation of a complex comprising P1 and P2, and detecting the presence of the complex of P1 and P2, where the presence of the complex indicates the presence of P2 in the sample; (6) removing (M2) a polypeptide from a biological sample, by providing a biological sample comprising P1, contacting the biological sample with P2 under conditions suitable for formation of a complex comprising P1 and P2, and removing the complex from the sample; (7) treating (M3) or preventing a disease or disorder involving altered levels of (I), by administering a molecule that modulates the function of (I) to a subject; (8) an isolated NOVX polypeptide (VI) selected from: (i) a sequence encoded by a nucleic acid sequence (S) of 374, 486, 376, 479, 474, 404, 321, 413 or 472 base pairs (bp), given in the specification; (ii) a variant of the amino acid sequence encoded by (S), where one or more amino acids residues in the variant differs from the amino acid sequence of the mature form, provided that the variant differs in no more than 15 % of the amino acid residues from the amino acid sequence; (iii) a mature form of the amino acid sequence encoded by (S); and (iv) a variant of the mature form of the amino acid sequence encoded by (S), where one or more amino acids residues in the variant differs from the amino acid sequence of the mature form, provided that the variant differs in no more than 15 % of the amino acid residues from the amino acid sequence of the mature form; (9) an isolated nucleic acid (VII) selected from: (i) (S); (ii) a nucleotide sequence differing by one or more nucleotides from (S), provided that no more than 20 % of the nucleotides differ from (S); and (iii) a fragment of (i) or (ii); (10) a vector (VIII) comprising (III) or (VII); (11) a cell (IX) comprising (VIII); and (12) an antibody (X) that binds immunospecifically to (I) or (VI). WIDER DISCLOSURE - Also disclosed are: (1) a nucleic acid molecule that differs from (S) due to the degeneracy of the genetic code; (2) an isolated antisense nucleic acid molecule hybridizable or complementary to (S) or its fragments, analogs or derivatives; (3) a nucleic acid molecule encoding NOVX proteins that contain changes in amino acid residues that are not essential for activity; (4) NOVX chimeric or fusion proteins; (5) variants of NOVX proteins that function either as agonists or antagonists; and (6) an immunoconjugate comprising (X) conjugated to a cytotoxic agent. BIOTECHNOLOGY - Preferred Complex: In (I), P1 or P2 is labeled. In (I), P1 comprises a region of amino acids of a polypeptide selected from a polypeptide given in the specification such as PPP1CC sufficient to allow P1 to bind P2, and P2 comprises a region of amino acids of the corresponding polypeptide given in the specification such as PPP1CC-NOV1, sufficient to bind P1. Preferred Kit: In (V), the reagent is selected from an antibody specific for (I), an antibody specific for P1 and an antibody specific for P2. Preferred Polypeptide: (VI) comprises the sequence of a naturally-occurring allelic variant of the sequence encoded by (S), where the allelic variant comprises a sequence that is the translation of a sequence differing by a single nucleotide from (S). The sequence of the variant comprises a conservative amino acid substitution. Preferred Polynucleotide: (VII) hybridizes under stringent conditions to (S) or its complement. Preferred Vector: (VIII) further comprises a promoter operably-linked to (VII). Preferred Antibody: (X) binds to (I) with higher affinity than it binds to the first or second polypeptide when the polypeptides are not complexed. (X) is a monoclonal or humanized antibody. Preparation: The polypeptides of (I) are prepared by standard recombinant techniques. ACTIVITY - Antidiabetic; Hypotensive; Hepatotropic; Cytostatic. MECHANISM OF ACTION -

Interaction of a vesicle trafficking-associated protein, a phosphatase I protein, or a calcium binding protein with a ligand inhibitor (claimed); Gene therapy. No biological data is given. USE - (I) is useful: (i) for identifying an agent which disrupts a polypeptide complex, preferably comprising at least one vesicle trafficking-associated protein; (ii) for inhibiting interaction of a vesicle trafficking-associated protein, a phosphatase I protein, or a calcium binding protein with a ligand; (iii) for identifying a polypeptide complex in a subject; and (iv) for determining altered expression of a polypeptide in a subject. A molecule that modulates (I) is useful for treating or preventing a disease or disorder involving altered levels of (I) (claimed). (I) is useful for identifying agents which modulate cellular process in which one or more members of (I) have previously been associated, for identifying agents and mechanisms that are involved in diabetes, and for preventing or treating disorders involving altered levels of (I). A NOVX polypeptide (VI) is useful for treating disorders associated with aberrant NOVX expression or activity such as disorders of renal and pancreas dysfunction, e.g., diabetes, hypertension, cirrhosis and cancer. (VI), a nucleic acid (VII) or an antibody (X) is useful in screening assays, detection assays (e.g., chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g., diagnostic assays, prognostic assays, monitoring clinical trials and pharmacogenomic), and in methods of treatment (e.g., therapeutic and prophylactic). (VI) is useful as immunogen to produce antibodies immunospecific for (VI), to screen for potential agonist and antagonist compounds, and as bait protein in a two-hybrid or three-hybrid assay. (VII) is useful in gene therapy, to express (I), to detect NOVX mRNA or a genetic lesion in a NOVX gene, and to modulate NOVX activity. (X) useful for detecting, isolating, and purifying (VI) and to monitor protein levels in tissue as part of a clinical testing procedure. ADMINISTRATION - (I) is administered by intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural or oral route. An isolated NOVX polypeptide (VI), a nucleic acid (VII) or an antibody (X) is administered by parenteral e.g., intravenous, intradermal, subcutaneous, oral (e.g., inhalation), transdermal, transmucosal or rectal route. No specific dosages are given. EXAMPLE - None given. (111 pages)

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